

GAGGAAAAAG ACAGGGGCCT GCTTGCCCAG CCATGCGAGG GATTCATGC CCACCTGCCC 420
 TCTGYCTGCC TCGCTGGAAT GTGGGCCCCCT GCTCCCCGTC AGGTTGTGCT GTCTCTGACC 480
 5 TATGTTTACA TCCCCGAGGG GTTTCTGCCT CCTCCCCACC CAGGTCAGGG TGTGGTCCAG 540
 CAGCTTGCTG TGGGGTGCTG ACATGIGTCA CCACTGCCCC CCTTGCCCCC GGGGGGTCA 600
 10 TGGTCTCCTC CTGGATGCTG CTCCTGAAT YTTTTTYYT GAWAAACCYT TTAMAATTAA 660
 AAAAAAAAAA AAAAACTCG A 681

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(2) INFORMATION FOR SEQ ID NO: 190:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

GCCTCAAGCC ACGCATATGA TAATTTCTG GAACATTCAA ATTCAGTGT TCTACAGCCA 60
 GTTAGTCTAC AAACCATTCG AGCAGCACCA TCAAACCAGA GTCTGCCACT TTTGTGTCATC 120
 30 GCTGGATGAT TGCTGGGCAA AGGTGGCCTT TTAGAGCTCT TAAAAGCCCA CAAAAGGCT 180
 ATTCGTAGAG CCACAGTCAA CACATTTGGT TATATTGCAA AGGCCATTGG CCTCATGATG 240
 35 TATTGGCTAC ACTTCTGAAC AACCTCAAAG TTCAAGAAAG GCAGAACAGA GTTGTACCA 300
 CTGTAGCAAT AGCTATTGTT GCAGAAACAT GTTCACCCTT TACAGTACTC CCTGCCTTAA 360
 TGAATGAATA CAGAGTTCCT GAACTGAATG TTCAAATGG AGTGTTAAAA TCGCTTTCCT 420
 40 TCTTGTTTGA ATATATTGGT GAAATGGGAA AAGACTACAT TTATGCCGTA ACACCGTTAC 480
 TTGAAGATGC TTTAATGAT AGAGACCTTG TACACAGACA GACGGCTAGT GCAGTGGTAC 540
 45 AGCACATGTC ACTTGGGGTT TATGGATTTG GTTGTGAAGA TTCGCTGAAT CACTTGTGTA 600
 ACTATGTATG GCCCAATGTR TTTGAGACAT CTCCTCATGT AATTCAGGCA GTTATGGGAG 660
 CCCTAGAGGG CCTGAGAGTT GCTATTGGAC CATGTAGAAT GTTGCAATAT TGTTTACAGG 720
 50 GTCTGTTTCA CCCAGCCCGG AAAGTCAGAG ATGTATATTG GAAAATTTAC AACTCCATCT 780
 ACATTGGTTC CCAGGACGCT CTCATAGCAC ATTACCCAAG AATCTACCAA CGATGATAAG 840
 55 RACACCTATA TTCGTTATGA ACTTGACTAT ATCTTATAAT TTTATTGTTW ATTTKGTGKT 900
 TAATGCACAS TACTTCACAC CTAAACTTG CTTTGATTG GTGATGTAAA CTTTTAAACA 960
 TTGCAGATCA GTGTAGGACT GGTCCATAGG GGAAGAGCTA GGAANTCCAT AGGC 1014
 60

(2) INFORMATION FOR SEQ ID NO: 191:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2779 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

TCGCAGCAGG GTGTGTCCAG ATGGTCAGTC TCTGGTGGCT AGCCTGTCTT GACAGGGGAG 60
15 AGTTAAGCTC CCGYTCTCCA CCGTGCCGGC TGGCCAGGTG GGCTGAGGGT GACCGAGAGA 120
CCAGAACCTG CTTGCTGGAG CTTAGTGCTC AGAGCTGGGG AGGGAGGTTT CGCCGCTCCT 180
20 CTGCTGTCTAG CGCCGGCAGC CCCTCCCGGC TTCACTTCTT CCCGACGCCC CTGCTACTGA 240
GAAGCTCCGG GATCCACGCA GCCGCCACGC CCTGGCCTCA GCCTGCGGGG CTCCAGTCAG 300
GCCAACACCG ACGCGCANTG GGAGGAAGAC AGGACCCTTG ACATCTCCAT CTGCACAGAG 360
25 GTCTTGCTG GACCGAGCAG CTCCTCTCTC CTAGGATGAC CTCACCTTCC AGCTCTCCAG 420
TTTTCAGGTT GGAGACATTA GATGGAGGCC AAGAAGATGG CTCTGAGGCG GACAGAGGAA 480
30 AGCTGGATTT TGGGAGCGGG CTGCCTCCCA TGGAGTCACA GTTCCAGGGC GAGGACCGGA 540
AATTCGCCCC TCAGATAAGA GTCAACCTCA ACTACCGAAA GGAACAGGT GCCAGTCAGC 600
CGGATCCAAA CCGATTGAC CGAGATCGGC TCTTCAATGC GGTCTCCCGG GGTGTCCCCG 660
35 AGGATCTGGC TGGACTTCCA GAGTACCTGA GCAAGACCAG CAAGTACCTC ACCGACTCGG 720
AATACACAGA GGGCTCCACA GGTAAGACGT GCCTGATGAA GGCTGTGCTG AACCTTAAGG 780
40 ACCGGGTCAA TGCTGCATT CTGCCACTGC TGCAGATCGA CCGGGACTCT GGCAATCTCT 840
AGCCCCTGGT AAATGCCCAG TGCACAGATG ACTATTACCG AGGCCACAGC GCTCTGCACA 900
TCGCCATTGA GAAGAGGAGW CTGCAGTGTG TGAAGCTCCT GGTGGAGAAT GGGGCCAATG 960
45 TGCAATGCCG GGTCTGCGGC GCTTCTTCCA GAAGGGCCAA GGGACTTGCT TTTATTTCCG 1020
TGAGCTACCC CTCTYTTTGG CCGCTTGCAC CAAGCAGTGG GATGTGGTAA GCTACCTCCT 1080
50 GGAGAACCCA CACCAGCCCG CCAGCCTGCA GGCCTGACT CCCAGGGCAA CACAGTCTCT 1140
CATGCCCTAG TGATGATCTC GGACAACTCA GCTGAGAACA TTGCACTGGT GACCAGCATG 1200
TATGATGGGC TCCTCCAAGC TGGGGCCCGC CTCTGCCCTA CCGTGCAGCT TGAGGACATC 1260
55 CGCAACCTGC AGGATCTCAC GCCTCTGAAG CTGCCGCCA AGGAGGGCAA GATCGAGATT 1320
TTCAGGCACA TCCTGCAGCG GGAGTTTTC GAGCTGAGCC ACCTTTCCCG AAAGTTCACC 1380
60 GAGTGGTGCT ATGGGCCTGT CCGGGTGTG CTGTATGACC TGGCTTCTGT GGACAGCTGT 1440

GAGGAGAACT CAGTGCTGGA GATCATTGCC TTTCATTGCA AGAGCCCGCA CCGACACCGA 1500
ATGGTCGTTT TGGAGCCCCT GAACAACTG CTGCAGGCGA AATGGGATCT GCTCATCCCC 1560
5 AAGTTCTTCT TAAACTTCCT GTGTAATCTG ATCTACATGT TCATCTTCAC CGCTGTGCCC 1620
TACCATCAGC CTACCCCTGAA GAAGCAGGCC GCCCCTCACC TGAAAGCGGA GGTGGAAAC 1680
10 TCCATGCTGC TGACGGGCCA CATCCTTATC CTGCTAGGGG GGATCTACCT CCTCGTGGGC 1740
CAGCTGTGGT ACTTCTGGCG GCGCCACGTG TTCATCTGGA TCTCGTTTAT AGACAGCTAC 1800
TTTGAAATCC TCTTCCTGTT CCARGCCCTG CTCACAGTGG TGTCCCARGT GCTGTGTTTC 1860
15 CTGGSCATCG AGTGGTACCT GCCCCTGCTT GTGTCTGCGC TGGTGTGGG CTGCTGAAC 1920
CTGCTTTACT ATACACGTGG CTTCAGCAC ACAGGCATCT ACAGTGTCTAT GATCCAGAAG 1980
20 CCCTGGTGAG CCTGAGCCAG GANMITGGCG CCCCGAAGCT CCTACAGGCC CCAATGCCAC 2040
AGAGTCAGTG CAGCCCATGG AGGGACAGGA KGACGAKGGC AACGGGGCCC AGTACAGGGG 2100
TATCTTGAA GCCTCCTTGG AGCTCTTCAA ATTACCATC GGCATGGCG AGCTGGCCTT 2160
25 CCAGGARCAG CTGCACTTCC GCGGCATGGT GCTGTCTGTG CTGCTGGSCT ACGTGTGTGT 2220
CACCTACATC CTGTGTCTCA ACATGTCTAT CGCCCTCATG AGCGAGACCG TCAACAGTGT 2280
30 CGCCACTGAC AGCTGGAGCA TCTGGAAGCT GCAGAAAGCC ATCTCTGTCC TGGAGATGGA 2340
GAATGGCTAT TGGTGGTGCA GGAAGAAGCA GCGGGCAGGT GTGATGCTGA CCGTTGGCAC 2400
TAAGCCAGAT GGCAGCCCSG ATGAGCGCTG GTGCTTCAGG GTGGAGGAGG TGAAGTGGC 2460
35 TTCATGGGAG CAGACGCTGC CTACGCTGTG TGAGGACCG TCAGGGGCAG GTGTCCCTCG 2520
AACTCTCGAG AACCTGTCC TGGCTTCCCC TCCCAAGGAG GATGAGGATG GTGCCTCTGA 2580
40 GGAAACTAT GTGCCGTCC AGCTCTCCA GTCCAAGTGA TGGCCAGAT GCAGCAGGAG 2640
GCCAGAGGAC AGAGCAGAGG ATCTTTCCAA CCACATCTGC TGGCTCTGGG GTCCCACTGA 2700
ATTCTGGTGG CAAATATATA TTTTCACTAA CTCAAAAAA AAAAAAAA AAAAAAAA 2760
45 AAAAAAAA AAAAAAGGC 2779

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(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

	ACCCGCTCCG CTCGGCTCCG CTCGGCCCCG CGCCGCCCGT CAACATGATC CGCTGCGGCC	60
	TGGCCTGCGA GCGCTGCCG TGGATCCTGC CCCTGCTCCT ACTCAGCGCC ATCGCCTTCG	120
5	ACATCATCGC GCTGGCCGGC CGCGCTGGT TGCAGTCTAG CGACCACGGC CAGACGTCCT	180
	CGCTGTGGTG GAAATGCTCC CAAGAGGGCG GCGGCAGCGG GTCCTACGAG GAGGGCTGTC	240
	AGAGCCTCAT GGAGTACCG TGGGTAGAG CAGCGGCTGC CATGCTCTTC TGTGGCTTCA	300
10	TCATCCTGGT GATCTGTTTC ATCCTCTCCT TCTTCGCCCT CTGTGGACCC CAGATGCTTG	360
	TCTTCCTGAG AGTGATTGGA GGTCTCCTTG CCTTGGCTGC TGTGTTCCAG ATCATCTCCC	420
15	TGGTAATTTA CCCCGTGAAG TACACCAGA CCTTCACCCCT TCATGCCAAC CSTGCTGTCA	480
	CTTACATCTA TAACTGGGCC TACGGCTTTG GGTGGGCAGC CACGATTATC CTGATYGGCT	540
	GTGCCCTTCTT CTTCTGCTGC CTCCCCAACT ACGAAGATGA CCTTCTGGGC AATGCCAAGC	600
20	CCAGGTACTT CTACACATCT GCCTAACTTG GGAATGAATG TGGGAGAAAA TCGCTGCTGC	660
	TGAGATGGAC TCCAGAAGAA GAACTGTTC CTCCAGCGCA CTTTGAACCC ATTTTITGGC	720
25	AGTGTTCATA TTATTAACT AGTCAAAAT GCTAAAATAA TTTGGGAGAA AATATTTTTT	780
	AAGTAGTGT ATAGTTCAT GTTTATCTTT TATTATGTTT TGTGAAGTTG TGTCTTTTCA	840
	CTAATTACCT ATACTATGCC AATATTTCTT TATATCTATC CATAACATTT ATACTACATT	900
30	TGTAAGAGAA TATGCACGTG AAACCTAACA CTTTATAAGG TAAAAATGAG GTTTCCAAGA	960
	TTTAATAATC TGATCAAGTT CTTGTTATTT CCAAATAGAA TGGACTCGGT CTGTTAAGGG	1020
35	CTAAGGAGAA GAGGAAGATA AGGTTAAAAG TTGTTAATGA CCAAACATTC TAAAAGAAAT	1080
	GCAAAAAAAA AGTTTATTTT CAAGCCTTCG AACTATTTAA GGAAAGCAAA ATCATTTCTT	1140
	AAATGCATAT CATTTGTGAG AATTTCTCAT TAATATCCTG AATCATTCAT TTCAGCTAAG	1200
40	GCTTCATGTT GACTCGATAT GTCATCTAGG AAAGTACTAT TTCATGGTCC AAACCTGTTG	1260
	CCATAGTTGG TAAGGCTTTC CTTTAAGTGT GAAATATTTA GATGAAATTT TCTCTTTTAA	1320
45	AGTTCTTTAT AGGGTTAGGG TGTGGGAAAA TGCTATATTA ATAAATCTGT AGTGTTTTGT	1380
	GTTTATATGT TCAGAACCAG AGTAGACTGG ATTGAAAGAT GGACTGGGTC TAATTTATCA	1440
	TGACTGATAG ATCTGGTTAA GTTGTGTAGT AAAGCATTAG GAGGGTCATT CTTGTCACAA	1500
50	AAGTGCCACT AAAACAGCCT CAGGAGAATA AATGACTTGC TTTTCTAAAT CTCAGGTTTA	1560
	TCTGGGCTCT ATCATATAGA CAGGCTTCTG ATAGTTTGCA ACTGTAAGCA GAAACCTACA	1620
55	TATAGTTAAA ATCCTGGTCT TTCTTGGTAA ACAGATTTTA AATGTCTGAT ATAAAACATG	1680
	CCACAGGAGA ATTGCGGGAT TTGAGTTTCT CTGAATAGCA TATATATGAT GCATCGGATA	1740
60	GGTCATATG ATTTTITACC ATTTGACTT ACATAATGAA AACCAATTCA TTTTAAATAT	1800

	CAGATTATTA TTTTGTAAGT TGTGGAAAAA GCTAATGTGA GTTTTCATTA TGAAGTTTTC	1860
	CCAATAAACC AGGTATTCTA AAAAAAAAAA AAAAAAACTN GAGGGGGGGC CCGGTACCCA	1920
5	ATT	1923
10	(2) INFORMATION FOR SEQ ID NO: 193:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2346 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:	
20	AGGCTCAGGG GGACACTCTC AAAATTACAC AGCTTTTAAC AGGTGGCAGA ATTGGGGTTC	60
	AGACCCAGAT CTGGGTTCAA GTCACATCATG GTGTGATTGC GGCATTCCCTT CCCGCATCTG	120
	GGCCTTGCCA TCTCTCTCTC CGAGTGGACA TGGAGAGGAC GGGGGCCCAG CAGCTGGATG	180
25	GCTGCAGGGG ATCAAGTCTT CTCTGGGGCT GGGCACGTAN AAGAGCATGT GGCTGGTGGA	240
	CGGCATGCCT GGCTCCTCAC CTGGCAGTCT GCCTGCCCTG CTAACGGGCT GTCTCTTGTT	300
30	CCCCTAGTGC CCTCGGCTAG CATGACCCGC CTGATGCGWT SCCGCACAGC CTCTGGTTCC	360
	AGCGTCATTC TCTGGATGGC ACCCGCAGCC GCTCCACAC CAGCGAGGGC ACCCGAAGCC	420
	GCTCCACAC CAGCGAGGGC ACCCGCAGCC GCTCGCACAC CAGCGAGGGG GCCCACCTGG	480
35	ACATCAACCC CAACTCGGGT GCTGCTGGGA ACAGNGCCCG GCCCAAGTCC ATGGAGGTCT	540
	CCTGCTAGGC GGCCTGCCCA GCTGCCGCC CCGGACTCTG ATCTCTGTAG TGGCCCCCTC	600
40	CTCCCCGCC CCTTTTCGCC CCCTGCCTGC CATACTGCGC CTAACGGT ATTAATCCAA	660
	AGCTTATTTT GTAAGAGTGA GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC	720
	TCTCCAAAGG CGGGGTGGCG GTGGACCAA GGAAGGAAGC AAGCATCTCC GCATCGCATC	780
45	CTCTTCATT AACCAGTGGC CGGTGCCCAC TCTCCTCCCC TCCCTCAGAG ACACCAAAT	840
	GCCAAAACA AGACGCTAC AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCCTGAGC	900
50	ATCTGGTTC AAACGGGTGC CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTTCCTCTTT	960
	AACTGAGGAG AAGCTGATCC AGTTTCCGGA AACAAAATCC TTTTCTCATT TGGGGAGGGG	1020
	GGTAATAGTG ACATGCAGGC ACCTCTTTTA AACAGGCAA ACAGGAAGGG GGAAAAGGTG	1080
55	GGATTCAATG CGAGGCTAGA GGCATTTGGA ACAACAAATC TACGTAGTTA ACTTGAAGAA	1140
	ACCGATTTTT AAAGTTGGTG CATCTAGAAA GCTTTGAATG CAGAAGCAA CAAGCTTGAT	1200
60	TTTTCTAGCA TCCTCTTAAT GTGCAGCAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG	1260

	ACAAAAATAT TTCAGCAAAC GTTGGGCATC ATGGTMTTGG AAGGCTTTAG TTCTGCTTTC	1320
5	TGCTCTCTCT CCACAGCCCC AACCTCCCAC CCCTGATACA TGAGCCAGTG ATTATTCCTG	1380
	TTCAGGGAGA AGATCATTTA GATTTGTTTT GCATTCCTTA GAATGGAGGG CAACATTCCA	1440
	CAGCTGCCCT GGCTGTGATG AGTGTCTTGG CAGGGGCCGG AGTAGGAGCA CTGGGGTGGG	1500
10	GGCGGAATTG GGGTTACTCG ATGTAAGGGA TTCTTGTGTG TTGTGTGAG ATCCAGTGCA	1560
	GTGTGATTT CTGTGGATCC CAGCTTGGTT CCAGGAATTT TGTGTGATG GCTTAAATCC	1620
	AGTTTTCAAT CTTGACAGC TGGGCTGGAA CGTGAAGTCA GTAGCTGAAC CTGTCTGACC	1680
15	CGGTCACGTT CTTGGATCCT CAGAACTCTT TGCTCTGTG GGGGTGGGG TGGGAAGTCA	1740
	CGTGGGAGC GGTGGCTGAG AAAATGTAAG GATTCCTGAA TACATATTCC ATGGGACTTT	1800
20	CCTTCCCTCT CTGCTTCTT CTTTCTCTGC TCCCTAACCT TTCGCCGAAT GGGGCAGCAC	1860
	CACTGACGTT TCTGGGCGGC CAGTGGGCT GCCAGGTTCC TGTACTACTG CCTTGTACTT	1920
	TTCATTTTGG CTCACCGTGG ATTTTCTCAT AGGAAGTTG GTCAGAGTGA ATTGAATATT	1980
25	GTAAGTCAGC CACTGGGACC CGAGGATTTT TGGGACCCCG CAGTTGGGAG GAGGAAGTAG	2040
	TCCAGCCTTC CAGGTGGCGT GAGAGGCAAT GACTCGTTAC CTGCCGCCCA TCACCTTGGA	2100
30	GGCCTTCCCT GGCCTTGAGT AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGAGTACGGA	2160
	TGGGAACTA TTGTGCACAA GTCTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA	2220
	TTTCCAGACC AATAAATTTG TAACTTTGCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2280
35	AAAAAAAAAA AAAAAAACT CGAGGGGGC CCGTACCCAA TTCGCCGTAT ATGATCGTAA	2340
	ACAATC	2346
40		

(2) INFORMATION FOR SEQ ID NO: 194:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3054 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

	TATCTGAACC ACCCTTTATT CTACATATGA TAGGCAGCAC TGAAATATCC TAACCCCTTA	60
55	AGCTCMAGGT GCCCTGTGGN ACGAGCAACT GGAATATAGC AGGGCTGGGC TCTGTCTTCC	120
	TGTCATAGG CTCACTCTTT CCCCCAAATC TTCCTCTGGA GCTTTGCAGC CAAGGTGCTA	180
60	AAAGGAATAG GTAGGAGACC TCTTCTATCT AATCCTTAAA AGCATAATGT TGAACATTCA	240

	TTCAACAGCT GATGCCCTAT AACCCCTGCC TGGATTTCCTT CCTATTAGGC TATAAGAAGT	300
	AGCAAGATCT TTACATAATT CAGAGTGGTT TCATTGCCCTT CCTACCCTCT CTAATGGCCC	360
5	CTCCATTTAT TTGACTAAAG CATCACACAG TGGCACTAGC ATTATACCAA GAGTATGAGA	420
	AATACAGTGC TTTATGGCTC TAACATTACT GCCTTCAGTA TCAAGGCTGC CTGGAGAAAG	480
10	GATGGCAGCC TCAGGGCTTC CTTATGTCTT CCACCACAAG AGCTCCTTGA TGAAGGTCAT	540
	CTTTTCCCC TATCCTGTC TCCCCCTCCC CGCTCCTAAT GGTACGTGGG TACCCAGGCT	600
	GGTCTTGGG CTAGGTAGTG GGGACCAAGT TCATTACCTC CCTATCAGTT CTAGCATAGT	660
15	AAACTACGGT ACCAGTGTTA GTGGGAAGAG CTGGGTTTTC CTAGTATACC CACTGCATCC	720
	TACTCCTACC TGGTCAACCC GCTGCTTCCA GGTATGGGAC CTGCTAAGTG TGAATTACC	780
20	TGATAAGGA GAGGGAAATA CAAGGAGGGC CTCTGGTGTT CCTGGCCTCA GCCAGCTGCC	840
	CACAAGCCAT AAACCAATAA AACAAGAATA CTGAGTCAGT TTTTATCTG GGTTCCTTC	900
	ATTCCCACTG CACTTGGTGC TGCTTTGGCT GACTGGGAAC ACCCCATAAC TACAGAGTCT	960
25	GACAGGAAGA CTGGAGACTG*TCCACTTCTA GCTCGGAACT TACTGTGTAA ATAAACTTTC	1020
	AGAACTGCTA CCATGAAGTG AAAATGCCAC ATTTTGCTTT ATAATTCTA CCCATGTTGG	1080
30	GAAAACTGG CTTTTTCCCA GCCCTTTCCA GGCATAAAA CTCAACCCCT TCGATAGCAA	1140
	GTCCCATCAG CCTATTATTT TTTTAAAGAA AACTTGCACT TGTTTTCTT TTTACAGTTA	1200
	CTTCCTTCTT GCCCCAAAAT TATAAATCTT AAGTGTA AAAAGTCTTA ACAACAGCTT	1260
35	CTTGCTTGTA AAAATATGTA TTATACATCT GTATTTTTAA ATTCTGCTCC TGAAAAATGA	1320
	CTGTCCCATT CTCCACTCAC TGCAATTGGG GCCTTTCCCA TTGGTCTGCA TGTCTTTTAT	1380
40	CATTGCAGGC CAGTGGACAG AGGGAGAAGG GAGAACAGGG GTCGCCAACA CTTGTGTTGC	1440
	TTTCTGACTG ATCCTGAACA AGAAAGAGTA ACACTGAGGC GCTCGCTCCC ATGCACAACT	1500
	CTCCAAAACA CTTATCTTCC TGCAAGAGTG GGCTTTCCAG GGTCTTTACT GGAAGCAGT	1560
45	TAAGCCCCCT CCTCACCCTT TCCTTTTTTC TTTCTTTACT CCTTTGGCTT CAAAGGATTT	1620
	TGAAAAAGAA ACAATATGCT TTACTCAT TTTCAATTTT TAAATTGCA GGGGATACTG	1680
50	AAAAATACGG CAGGTGGCCT AAGGCTGCTG TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT	1740
	TACAAGATAA AAAACGAATC CCTAAACAA AAAGAACAAT AGAACTGGTC TTCCATTTTG	1800
	CCACCTTTC TGTTCATGAC AGCTACTAAC CTGGAGACAG TAACATTTCA TTAACCAAAG	1860
55	AAAGTGGGTC ACCTGACCTC TGAAGAGCTG AGTACTCAGG CCACTCCAAT CACCCTACAA	1920
	GATGCCAAGG AGGTCCCAGG AAGTCCAGCT CCTTAACTG ACGCTAGNCA ATAAACCTGG	1980
60	GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT CCATCTGTGA GGTGACAGGC AAGGATGAAA	2040

	GACAAAGAAG GAAAAGAGTA TCAAAGGCAG AAAGGAGATC ATTTAGTTGG GTCTGAAAGG	2100
	AAAAGTCTTT GCTATCCGAC ATGTACTGCT AGTACCTGTA AGCATTTTAG GTCCCAGAAT	2160
5	GGAAAAAAA ATCAGCTATT GGTAATATAA TAATGTCTT TCCCTGGAGT CAGTTTTTTT	2220
	AAAAAGTTAA CTCTTAGTTT TTAATTGTTT AATTCTAAAA GAGAAGGGAG CTGAGGCCAT	2280
10	TCCCTGTAGG AGTAAAGATA AAAGGATAGG AAAAGATTCA AAGCTCTAAT AGAGTCACAG	2340
	CTTTCCCAGG TATAAACCT AAAATTAAGA AGTACAATAA GCAGAGGTGG AAAATGATCT	2400
	AGTTCTGAT AGCTACCCAC AGAGCAAGTG ATTTATAAAT TTGAAATCCA AACTACTTTC	2460
15	TTAATATCAC TTTGGTCTCC ATTTTCCCA GGACAGGAAA TATGTCCCCC CCTAACTTTC	2520
	TTGCTTCAA AATTAAAAATC CAGCATCCCA AGATCATTCT ACAAGTAATT TTGCACAGAC	2580
20	ATCTCCTCAC CCCAGTGCCT GTCTGGAGCT CACCCAAGGT CACCAAACAA CTGGGTTGTG	2640
	AACCNAACTG CCTTAACCTT CTGGGGGAGG GGGATTAGCT AGACTAGGAG ACCAGAAGTG	2700
	AATGGGAAAG GGTGAGGACT TCACAATGTT GGCCTGTCAG AGCTTGATTA GAAGCCAAGA	2760
25	CAGTGGCAGC AAAGGAAGAC TTGGCCCAGG AAAACCTGT GGGTTGTGCT AATTCTGTCT	2820
	CAGAAAATAG GGTGGACAGA AGCTTGTTGG GTGCATGGAG GAATTGGGAC CTGGTTATGT	2880
30	TGTTATTCTC GGACTGTGAA TTTTGGTGAT GTAAAACAGA ATATTCTGTA AACCTAATGT	2940
	CTGTATAAAT AATGAGCGTT AACACAGTAA AATATTCAAT AAGAAGTCAA AAAAAAAAAA	3000
	AAAAAACTCG AGGGGGGGCC CGGTACCCAA TTNCCAAAT AGAGATNGTA TTAC	3054
35		

(2) INFORMATION FOR SEQ ID NO: 195:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

	GGCAGAGCTC GTGGCCGNAA CTTTTTCTGC TCCTGGCTGC CACCTACTGG CTGGCCGCGG	60
50	CCCTGGCCTG GGCCTGCACC AGCCTGCGNG CGGGCTCCCA CAGCAGCCCC CTTCCAAGCA	120
	GCGTCCCCAC ACCGCGCACC TTCTGCGGGA ACGTGCTCGC CGTGCCGGGG ACCATATGGA	180
55	CGGAAGGCTT TGTGCTCACC TACAAGCTGG GTGAGCAGGG TGCCAGCAGC CTGTTGATCC	240
	TCTTGCTCC TGCTGGAGCA CGAGCGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG	300
	TGTGGGTGCT GTGGTCTGCT CCATCGCTGG CTCCTCCCTG GGTGGGACCT TGCTGGCCAA	360
60	GCACTGAAA CTGCTGCCTC TGTGAGGTGG GTGCTGCGCT TCGCCTCGG GGGCCTAGCC	420

5 TGTCACTG CCTTGGTCTT CCACCTTGA CACCTGGGG GCCAGCATGG ACGCTGGCAC 480
 AATCTTGAGA GGGTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GARGCCTGGT 540
 CACCACAGTC ACCTTCACTG GGAATGATGC GCTGCAGCCA GCTGGCCCCC AGGGCCTTGC 600
 AGGCCACACA CTACAGCCTT CTGGCCACGC TGGAGCTGCT GGGGAAGCTG CTGCTGGGCA 660
 10 CTTTGGSCGG AGGGCCTGGC TGATGGGTTG GGGCCACATC CCTGCTTCTT GCTCCTGCTC 720
 ATCCTCTCTG CCTTTCCTGT TCTGTACCTG GACCTAGCAC CCAGCACCTT TCTCTGAGCT 780
 GAGTGGCTGG AGTGGTCAAT AAAGCCACAT GTGCTGTGG CCCAAAAAA AAAAAAAA 840
 15 AAAAAAAA AAAAAAATG GAGGGGGGC CCGGTACCCA AATCGCCGA TATGATCGTA 900
 AACAATC 907

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(2) INFORMATION FOR SEQ ID NO: 196:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

GGCACGAGGA GGGACAGGA GTGGCAAGG GGAAGAAGCA GCTTATTTGA CTAACCAGCC 60
 35 CCTCTGTGGT CCACGAGCT CTTGGCTTGG TGGGAGGGCT CTCAATCAGC AGGGCCCCAG 120
 KAGGGCAAGA AGAAGTGGG CAAAGCCTGG CGCTCGGCG CGGTGCGGC AGCTTTGCM 180
 TCTGGAGCCA CGCTCTCTCC AGGCCATGCT CTTGAACTT GGAAATGTCA ACCGAGCCC 240
 40 TTAACACCAG CCTCCAGCA TCTAATAGAC TTGAATCTAC TCTAAACGAA TATTTAATCC 300
 AACCTCAACT ACATTGTAGC TCAGTCCAAC GACTAACCTT GAAATGGGG TGTTCAGCC 360
 45 TTCAGCGAGA TGCCCAAGCG GTCCCTGGG GGCTGTGGCA GCGGGCTTAT CCTTCTCTGT 420
 TGCCAACCTT GCCGTCCGAC CTCCTCCGCC CCCATGCGGT GACCCCGTCC GTGTCTGTGT 480
 CTGTCCATAC GTGTGAGTCC AGCTAAAAG ACAAACAGA ACCCGTGGG CCAGCTCGGA 540
 50 AGGTGCGTGG AGAAGGCTCC GACGTCTCCG AAGTGCAGCC CTTGGGATGG CATTCGGTTG 600
 TGTGCCTTAT TCCTGGAGAA TCTGTATACG GCTCGCTAT AAGAAATATA GCCTCTTCAT 660
 55 GCTGTATTAA AAGGACTTTT AAAAGCAAAA AAAAAAAA AAAAACTGA GGGGGGGCCC 720
 GGTACCCAAT TCGCCCAATA GTGAGTCGTA TTACAATTCA CTGGCCGTC STTTAACAA 780
 CGTCGTGAAC TGGGAAAACC CTGGCGTTTA CCAACTTAA TCGCTTGCA GCACATCCC 840
 60

	CTTTGCGCCAG CTGGCGTTAA TAGCGAAAAA NGCCCCGACC CGAATCGCCC TTCCCAACAG	900
	TTTGGCGCAGC CCTGAATGGC GAAATGGCAA ATTGTAAGCG TTTAATATTT TKKTTAAAT	960
5	TCCNCGTTWA AWTTTTTGT TAAATCARCT CAATTTTTTT AACCCAATAA GSCCGAAATC	1020
	CGGCAAATCC CCYTTATTAA TTCCAAAAAA ATAAACCSAA AAWGGGTTTG AATTTTTTKT	1080
	TTCCCCAYTT TTGGAAACAA AWTYCCCCCT TTTTAAAAAA GTTGGAACCC CCAMCCYTCC	1140
10	AAAGGGGAAA AAACSYTTTT YTGCGGGGNA ANGGGGCCCC CNTACTTTNA ACAYCCCCCC	1200
	CCAAWCAATT TTTTTGGGG GTCCCNAAAG GTCCCCCTAA AANCTTTTTT CGGAACCCNA	1260
15	AGGGGANCCC CCCATTTAAA ATTTTNGGTN	1290
20	(2) INFORMATION FOR SEQ ID NO: 197:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1020 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:	
30	GGTGTGCGTG GATGGTCGTG TAGGTGAGTT TTACCAAGGA TTATGGTAAC AAATGAGTGA	60
	GACCTCTATG GAGAAATAT TGAAGNNCAT TAAAGAAGAC CTCATANTAG GAGAGAATGT	120
	SCTTTGGAGG ATTTGTATTG AGCTTTTACA GTATTCATTT TTCAACTCAA GGCAATGGCT	180
35	TTCTACACCA ACTCTAATCC ATAAACGGGT CTTATGACAT CTATGAAGTA GTAGCAAGAC	240
	ATGCTTAGTG TGTATTTCTC TCTTTGAGAC ACTGTAATTT CTACCAGAAA TTTCAGAGC	300
40	ATTATGTAGG TAGAAAAAA TGCAAGCAAG CTGTTAAAGA TCTTGATCC CATTATATAG	360
	TATGTATAGC TGAAATCTGT AATCAATCA CTTTTCTCT TTTATCCTCT AACCAAAAAA	420
45	TTGTTTAATT TTGCATCCCA AATGTTTTTA ATCTTTGTAT ATTTTTTAAA AAYCCTTTTC	480
	TCCTCATCAT TGCCTTTTTT GTGGTTGTAA ATAGACTTAC TTGCACTTTG AAGATGAGTT	540
	ACTCCTGTG ATCTTACAAA TATGTGATAT GGTAAATTTT ATAACAGATG TCAGTTTGA	600
50	ACCAAGAATT GGTGATTTGT TTATAAGAAA AAAACTGGCT TCATTTCTGT GAAATGCTC	660
	TTTGAAAATT TCTTTTACA CGTGTAAGCC AACTGAGATA CCGTGATGGT GTTGATTTCT	720
	TTCAATGATG CTTACCATCT ATTTTAGCCA CTGAGCCTTT TATTATTTGT CTATTTGTAA	780
55	AGTTTATTTG TCTTAATCA TTTAATAAAT ATACTGTTTA TCTGTTTCTG AATGGGGACT	840
	GAACTTTTTG GATATTGATA TTGATTTGAA AATATTTTGG AATTTTTTCT ACTTGAAATT	900
60	TTAGAAATCT AATKGAAAAT TCTATAATGT ACTGAAAGTA WGGTTGTGTA CAGTGAKCAC	960

TCTCTAATAA TATGATGNCT TGCCCTAAAN GAGGNGGGAC ATGTCCCACT TTCCACCACG 1020

5

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

15

AATTCCCGAA GCTGAGGGTT GTGTGCCNTC GGGCGAGCCA AGTCTTTTGA CCGGACCCCTT 60
CCCGGCGCAG AAGANCTGAA GTTGATTTGA GAGCCTGTKT TTGGGGTTTRA GCCGAGCTGC 120
20 TCGGGGCTTY GTCGCCGCC AGGACACAAG YTACTTGCAA CGGGGCGGCG CCTGGCTTAT 180
GATGTTCCCTC AACCCAGGGG CGGCCTCTGC CCTCTACTCG TGCCAGGCC ACTTGCCAGG 240
25 CAGGAGCCCT CCCCAAGCCT TCAGGCTGCTG TCGGAGTCAC CTGTTGGAAT GGACTAAAAG 300
GACCCCTGTG TGGGAACAGG TGCTCCAAAC ACCCTGCTGC TGGCTGCCAG GCAGGCCCTC 360
TGAAGGGAA GGGGCAGGAC TCATCAGGAC CTCCTGGAC CCTGCAGGGC AGGCAGTTGG 420
30 CCCGAGCCCA AGCATTTGGC TCTGCTTGCC CCAAGGGGAC AGGAAGCCTC TTGGGCCTCT 480
TCCCTTCCTG GACAAGGCC CCTGCCTTTG CCTCACATAA ACTG 524

35

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGATACAAG GAAGGGTGAT CATCATCTGT CACCATGCAA TTCCTGCTCA CAGCCTTTCT 60
50 GTTGGTGCCA CTTCTGGCTC TTTGTGATGT CCCCATATCC CTAGGCTTCT CCCCTCCTA 120
GAAGGGCTTC TTGATAGATT AGAAAATAAG AATGAGTGAC ATTTCCTATG TGCATATAAG 180
AAGGAGCCAC AAGACATGTC TTTTAAATAA AAGGACAGTG TCCATCCTTT TAGCTGCCGA 240
55 ATAGAACCTT GGTCTCATCC TCCTGGAGCT AGGSCTTAAA ACAGCTTCTG TGTTTCTSAT 300
TKGTCTCART GTTTTGCCAA GGTTTTATTC GG 332

60

(2) INFORMATION FOR SEQ ID NO: 200:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

CCAGGGAAGC CCCARGCCTG TCCTGAATTG ACATCAGTGC TTCCCTGAAC TGCCTCCCCC 60
15 ACCCCTGGGC ATTATCCCAG GAAACTTATG TTTTCTAGAA GCTAAGCAGC TGCTGGGACT 120
CAGGGACTGG TGCAGGTAGG CTGAGTGGCA GCTCAGTCCT AGAAGGTCTC TGAAGATCTG 180
GACTGAGGAC CYTGCTACTC CCCAAGCCAG AGCCCATCAG CCAGGCCTGC TGTGAGCCAC 240
20 CTGCCTGTGG AGTGCTGAGC TCAACCAAAG GCTGGCAAGC TCTGGGCCTC ATTTAAGGGA 300
TTCTGATGAG CCGATGGGCC CTGGAGGCAG CCCATTAAAG CATCTGGCTC GTTTTGGAA 360
25 AAAAAAAAAA AAAAAG 376

30

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40 CCCAGTATAT TTCTATAACA TTTATTTTAG TGAACCTATA ATGTTTCTTT GTATTAAATT 60
ATTAGATTAT ATCTTTAGAT AATATTGTTA CTNAATTAGT AGGTAATATA TATTTTATTC 120
AAAAATAAAT TGTGCATCTA ATGTCTACCA ATTAATGTAC TTGTAGATGT ATCTTATCTT 180
45 AACTTGAGTC TTTGCTGCCC CTAATGAGGT GTGAAGGACT CTTCTCCCTT GGGGAAGTTT 240
TTCTTTTTC A GGAGGGAGGA GGGCTTTCCC AGGTAATGTG TCTAGAGTGT TGGGCAGAA 300
50 AATCTGGGAC CACACCACAC CAGTTCTCTC CTTAATCCAC GTCATTTGCC TTCTATCCCA 360
GCTATGTTTC CAGTGTCTTC TGGGTGTTTC CAAGAGCAAC AAGAAAYGAA TAAATCTCTG 420
KTGAGTGTGT TATTTGTTCT TCACTTTGT TTTACTGTA WTTTCTGAGT TTATGGGTGT 480
55 CTGTGAATTA AAAAGGAAAA GTRGAAATAA GTAAACTCA GGTGAAGGA AATATACATA 540
AATAAGATAA AGCTGACCTG TAGATATARR CAGGTTATAA RAGCTTAGAG TTGTCTAAGT 600
60 TGRGTGCAAA KTTTCTCTG ATCTTTCTGA TGCCGARACA AAAAAGGCAG TCATGTTTGT 660

WATGTGATTG GAATGGAACC CGARAAGAGA GCAYGCTGTG TTCTTGGGGA CAGGAAAGCT 720
TGYGTGCACC AAGTCTKAAC CACCACCTTC ATGGGACATA GRTTATGTGC TGGAACATAT 780
5 TTACACCCGG CCTGGCAGTA AACACTTGTA GTGTTGTGCA GTGGAAACGG TCATCTTCCG 840
CTAAAGCACG GCGTGTGTG CAGCGGAAAT GGTCACTCTGC TGCTAAAACA CAGCTTCCAT 900
10 CGTAATGTAT GCTCCTTACT CAAAGAGTGT GGTCCCAAAC AGCCTTTGGG AGGTCTCTCT 960
TGATTCATGG ATGAAACCTG GAACATCTTG AGGACTGAGT TAACCATAGG TCCTTAAATA 1020
ACTCTCCACA CGTTTTTCTT AGTTTATCTC TACATGCAGG GTGTGCAGCA GCCTGTTCAA 1080
15 AGTCATATTT TCTGGGAAAT ATTTCCAGTG TTTATTTGCA CTTTAGCCCA CTCTGTGTAG 1140
CCTTATTTCT TCTAACTCA CCATTAATCT GAATAATAGT CAAATTTAGG GG 1192
20

(2) INFORMATION FOR SEQ ID NO: 202:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

ATCTTGGGCT ATCTTTGACA GGGGATCTCT GCAAGTTGAT GCTTTCTACA AGTGAATATA 60
35 GTCAGTCCCC AAAGATGGAG AGCTTGAGTT CTCACAGAAT TGATGAAGAT GGAGAAAACA 120
CACAGATTGA GGATACGGAA CCCATGTCTC CAGTTCTCAA TTCTAAATTT GTTCTTGCTG 180
AAAATGATAG TATCCTGATG AATCCAGCAC AGGATGGTGA AGTACAAC TGTCAGAAATG 240
40 ATGACAAAAC AAAGGGAGAT GATACAGACA CCMGGGATGA CATTAGTATT TTAGCCACTG 300
GTTGCAAGGG CAGAGAAGAA ACGGTAGCAG AAGATGTTTG TATTGATCTC ACTTGTGATT 360
45 CGGGGAGTCA GGCAGTCCG TCACCAGCTA CTCGATCTGA GGCACTTTCT AGTGTGTTAG 420
ATCAGGAGGA AGCTATGGAA ATTAAAGAAC ACCATCCAGA GGAGGGGTCT TCAGGGTCTG 480
AGGTGGAAGA AATCCCTGAG ACACCTGTG AAAGTCAAGG AGAGGAAC TC AAAGAAGAAA 540
50 ATATGGAGAG TGTTCCGTTG CACCTTTCTC TGACTGAAAC TCAGTCCCA 589

55 (2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 847 base pairs
60 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

5
GGCACGAGCG CAAGCTGCTG GCCGCCATCA ACGCGTTCCG CCAGGTGCGG CTGAAACACC 60
GGAAGCTCCG GGAACAAGTG AACTCCATGG TGGACATCTC CAAGATGCAC ATGATCCTGT 120
10 ATGACCTGCA GCAGAATCTG AGCAGCTCAC ACCGGGCCCT GGAGAAACAG ATTGACACGC 180
TGGCGGGGAA GCTGGATGCC CTGACTGAGC TGCTTAGCAC TGCCCTGGGG CCGAGCAGCT 240
TCCAGAACCC AGCCAGCAGT CCAAGTAGCT GGACCCACGA GGAGGAACCA GGCTACTTTC 300
15 CCCAGTACTG AGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCAGCCTGAA CAAAGCACCT 360
CAAGTGCAAG GACCAAAGGG GGCCTGGCTT GGATGGGTTG GCTTGCTGAT GGCTGCTGGA 420
20 GGGGACGCTG GCTAAAGTGG GGAGGCCTTG GCCCACCTGA GGCCCCAGGT GGGAACATGG 480
TCACCCACAC TCTGCATACC CTCATCAAAA AACTCTCAC TATGCTGCTA TGGACGACCT 540
CCAGCTCTCA GTTACAAGTG CAGGCGACTG GAGGCAGGAC TCTTGGGTCC CTGGGAAAGA 600
25 GGGTACTAGG GGCCCGGATC CAGGATTCTG GGAGGCTTCA GTTACCGCTG GCCGAGCTGA 660
AGAACTGGGT ATGAGGCTGG GCGGGGGCTG GAGGTGGCGC CCCCTGGTGG GACAACAAAG 720
30 AGGACACCAT TTTCCAGAG CTGCAGAGAG CACCTGGTGG GGAGGAAGAA GTGTAAGTCA 780
CCAGCCTCTG CTCTTATCTT TGTAATAAAT GTTAAAGCCA GAAAAAAAAA AAAAAAAAAA 840
AAAAAAA 847
35

(2) INFORMATION FOR SEQ ID NO: 204:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

ACAAACATAC TCGCAGGAAG GAGTCTCATG CTGCCCGCAG CATCAGCGCA ACNCNTGGCC 60
50 GCCATCAACG CGTTCGCCCA GTGCGGCTG AAACACCGGA AGCTCCGGGA ACAAGTGAAC 120
TCCATGGTGG ACATCTCCAA GATGCACATG ATCCTGTATG ACCTGCAGCA GAATCTGAGC 180
55 AGCTCACACC GGGCCCTGGA GAAACAGATT GACACGCTGG CGGGGAAGCT GGATGCCCTG 240
ACTGAGCTGC TTAGCACTGC CTTGGGGCCG AGGCAGCTTC CAGAACCCAG CCAGCAGTCC 300
AAGTAGCTGG ACCCACGNAG GAGGAACCAG GCTACTTTCC CCAGTACTGA GGTGGTGGAC 360
60

ATNCGTCTCT TGCCACTCCN TGNACCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC 420
 AAAGGGGGCC CTGGCTTGGA GTGGTTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC 480
 5 TAAAGTGGGK AGGCCTTGGC CCACCTGAGG CCCCAGGTGG GAACATGGTC ACCCCCACTC 540
 TGCATACCCT CATCAAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT 600
 TACAAGTGCA GCGACTGGA GGCAGGACTC CTGGGTCCCT GGGAAAGAGG GTAGTAGGGG 660
 10 CCGGATCCA GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT 720
 GAGGCTGGG CGGGCYGGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATT 780
 15 TTCCAGAGCT GCAGAGAGCA CCTGGTGGG AGGAAGAAGT GTAACCTACC AGCCTCTGCT 840
 CTTATCTTTG TA 852

20

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 1354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GATTGGGCAC GAGGCTTGCT GGAGCAGGAG AAGTCTCTRG CCGGCTGGGC ACTGGTGCTG 60
 GCASGARCTG GCATTGGACT CATGGTGCTG CATGCAGAGA TGCTGTGGTT CGGGGGGTGC 120
 35 TCGGCTGTCA ATGCCACTGG GCACCTTTCA GACACACTTT GGCTGATCCC CATCACATTC 180
 CTGACCATCG GCTATGGTGA CGTGGTGCCG GGCACCATGT GGGCAAGAT CGTYTGCTG 240
 40 TGCACTGGAG TCATGGGTGT CTGCTGCACA GCCCTGCTGG TGGCCGTGGT GGCCCGGAAG 300
 CTGGAGTTTA ACAAGGCAGA GAAGCACGTG CACAACITCA TGATGGATAT CCAGTATACC 360
 AAAGAGATGA AGGAGTCCGC TGCCCGAGTG CTACAAGAAG CCTGGATGTT CTACAAACAT 420
 45 ACTCGCAGGA AGGAGTCTCA TGCTGCCCGC AGGCATCAGC GCAANCTGCT GGCCGCCATC 480
 AACGCGTTCC GCCAGGTGCG GCTGAAACAC CGGAAGCTCC GGAACAAGT GAACTCCATG 540
 50 GTGACATCT CCAAGATGCA CATGATCCTG TATGACCTGC AGCAGAATCT GAGCAGCTCA 600
 CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CTTGACTGAG 660
 CTGCTTAGCA CTGCCCTGGG GCCGAGGCAG CTTCAGAAC CCAGCCAGCA GTCCAAGTAG 720
 55 CTGGACCCAC GAGGAGGAAC CAGGCTACTT TCCCCAGTAC TGAGGTGGTG GACATCGTCT 780
 CTGCCACTCC TGNACCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC AAAGGGGGCC 840
 60 CTGGCTTGGA GTGGTTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC TAAAGTGGGK 900

AGGCCTTGGC CCACCTGAGG CCCAGGTGG GAACATGGTC ACCCCCACTC TGCATACCCCT 960
CATCAAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT TACAAGTGCA 1020
5 GGCGACTGGA GGCAGGACTC YTGCGTCCCT GGGAAAGAGG GYACTAGGGG CCCGGATCCA 1080
GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT GAGGCTGGGG 1140
10 CGGGGCTGGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATTT TTCCAGAGCT 1200
GCAGAGAGCA CCTGGTGGGG AGGAAGAAGT GTAACCTACC AGCCTCTGCT CTTATCTTTG 1260
TAATAAATGT TAAAGCCAGA AAAAAATAAA AAAAAAAAAA AAAAAACTCG AGGGGGGGCC 1320
15 AGACCCAATC TCCCTATAGT AAGNCGCCNN ANAN 1354

20

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

30 TCCCCAGGTG CACAGCCAGG GCCCTCCTGT CTGAGGAGA ATTCACAGCT GGTGTGGGAC 60
TCAGCCCCCTA GNCCATTCAA AGCCTTAATG TTGTAATCAT ATCTTACGTG TTGAAGACCT 120
35 GACTGGAGAA ACAAATGTG CAATAACGYG AATTTTATCT TAGAGATCTG TGCAGCCTAT 180
TTCTGTCACA AAAGTTATAT TGTCTAATAA GAGAAGTCTT AATGGCCTCT GTGAATAATG 240
TAACTCCAGT TACACGGTGA CTTTAAATAG CATACAGTGA TTTGATGAAA GGACGTCAAA 300
40 CAATGTGGCG ATGTCGTGGA AAGTTATCTT TCCCGCTCTT TGCTGTGGTC ATTGTGTCTT 360
GCAGAAAGGA TGGCCCTGAT GCAGCAGCAG CGCCAGCTGT ANATAAAAAA TAATTCACAC 420
45 TATCAGACTA GCAAGGCACT AGAACTGGAA AAGACCACAG AAAACAAAGA ATCCAACCCT 480
TTCATCTTAC AGGTGAACAA ACTGTGATGA TGCACATGTA TGTGTTTGTG AAGCTGTGAG 540
CACCCTAACA AAATGTAAAT TTGCCATTAT TAGGAAGTGC TGGTGGCAGT GAAGAAGCAC 600
50 CCAGGCCACT TGACTCCCAG TCTGGTGGCC TGTCTACACC AGACAACACA GGAGCTGGGT 660
CAGATTCCCC TCAGCTGCTT AACAAAGTTC CTCGAACAGA AAGTGCTTAC AAAGCTGCCT 720
55 TCTCGGATAC TGAAAGGTCG AGTTTCTGA ACTGCACTGA TTTTATTGCA GTTGAAAAAA 780
AAAAAAGCT ATTCCAAAGA TTTCAAGCTG TTCTGAGACA TCTTCTGATG GCTTTACTTC 840
CTGAGAGGCA ATGTTTTTAC TTTATGCATA ATTCAATTGTT GCCAAGGAAT AAAGTGAAGA 900
60

AACAGCACCT TTTAATATAT AGGTCTCTCT GGAAGAGACC TAAATTAGAA AGAGAAAAC 960
GTGACAATTT TCATATTCTC ATTCTTAAAA AACACTAATC TTAAC TAACA AAAGTTCTTT 1020
5 TGAGAATAAG TTACACACAA TGGCCACAGC AGTTTGTCTT TAATAGTATA GTGCCTATAC 1080
TCATGTAATC GGTACTCAC TACTGCCCTT AAAAAAAAA ACCAGCATAT TTATTGAAAA 1140
CATGAGACAG GATTATAGTG CCTTAACCGA TATATTTTGT GACTTAAAA ATACATTTAA 1200
10 AACTGCTCTT CTGCTCTAGT ACCATGCTTA GTGCAAATGA TTATTTCTAT GTACAACTGA 1260
TGCTTGTCTT TATTTTAATA AATTATCAG AGTGAAAAA AAAAAAAAAA AAAAAAAAAA 1320
15 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGAA NAAAAANA 1378

20 (2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

30 AANCCACTGC ANTTTAAACC CCCTCCCTC CAAGAAAGTT CACAACCGGC CATGGATGAC 60
CCTCATTTTA GATGGGCNC AATATTAAAG ATGGACTGRG GMCCCCARAG ACTGACCCCT 120
GAAAGGGGA CTCAGAAGAA AGATCCTGA CATTGCCMAA CATGCTGGGC TTGTCCAACA 180
35 CAGTGATGCG GCTCATCGAG AARCGGCTT TCCMAGGACA AGTACTTAT GATAGGTGGG 240
ATGCTGCTGA CCTGTGTGGT CATGTTCTC GTGGTGCACT ACCTGACATG AGCCAGCCAC 300
40 GCTCAGTGGC TGAACAGCAT TCCCACAGCC TGCAAGTGTG TGTGTGTGTG AAAGAGAGAG 360
GGGGCCAGA GGCCGCTTT TGAATGTTT GCCTGTCTGA ACTGTGAAGA CACTTGGGAG 420
TGATTGTGGT CTAATTTCCA ACCTGCTCTG TTTTCTGTGA CATCTGGAG GGGAGCTAG 480
45 TGCCAMCACC ATGCGCGGTG CTTAGGAAAT GAAAGAAGTC CCGGTCTGT CTCTCTCACT 540
CTCGCTCTCA MTGGGGGAGG GAAAGAATGG CTTGGTGGC TTTGTTTACA CAGCTGATGC 600
50 GTGSCCTGGG AAGGTGTCCA CAGTGAGCCC TGTGTGCAGG ACTGTCCACN ACGTTTACA 660
CCTGTGACAC ATCAGGCCTT TCTGGCTCCT GATAGGTGG AGCAAAAGTG GAAAGGAAAG 720
GAAAGAGGCY TTTTCTTACA GCCATTATAT TAAATAGTAG GTCGATTAC ATCTCGTGC 780
55 TCCTGGCCAC CCTCCCTGT GCCTCAGTGA CATGTAGATG ACTGACTGCC AATACTTGT 840
ACCATTCCTT GGAAGCAGCT ACCTAGGGGA AACAAGATGT AGTGCTATTG CCGATAACAA 900
60 GTAAGATTTT CCACACTACA GCTGGGTGTT TCTCTTTTCT AAAGTGAGGC CAGTGTATT 960

1020 TCCCGGGAGT GTTCAGTCTT GACCCTAGTC ACTGATTTTT TCTAGTTGTT AATAGAGTGG
1080 TTGGGCTTTT AAGGTTTCAGA GACTGTGGGC TTGGGCACCT GCGCCCAGGG STTTTGTGGG
5 GGCCTTIGCC CCTTAGRAAA GTAGCTTTTA GGGGCAAAGA TTTGTTGATT TTCCCCATTA 1140
CAGTCTTCAG CTCNAGGGTT TTAAAA 1166

10

(2) INFORMATION FOR SEQ ID NO: 208:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

TACTTCTAGG ATTATAAGGA ATTAACATTG AGATGACATT TCCATTGAG AAGGAAAATA 60
25 GTTGCTTTCA GTGCCTTTA TTTGATTCTT GGAGAGAGCA GACTCGCACS AACATTCAAC 120
CCCAGCGCTG ATATGACAGT AATCCTCAGA GGCAGAGCCC AGCACAAAAC AGCAATGCTA 180
GAAAGTTACA ATTGGAAAGT TTCCTGCCAG CTTCGGGAAT GACACTGCAA AGCTGATGCC 240
30 AGAAACTGCC AGRGTAATTC TCCTCATTAC TGCTCTACCC ACCCACTTTC AGCTCCCCAA 300
ATTAAGTAGT GCAGTTGACT AATTCTCTTT ACCTTTATCA TTTARGGTGA RGCATTGCAC 360
35 AAAAAGTCTC GACTTTGCCA TATAAGGGCT GTGGTTCTCT GTGGTCCCCT GGATAAGAGG 420
CATCACCATT ATCTGGAAC ATGCAGTAAA TGCAGATTNT TCATCTTCTC CCCAGACCTC 480
CTGAGTTAGA AATTCACAAG TTCTCCAGGT GATCTCATACT ATGCTAAAAGT TTGAGAACCA 540
40 TTGAGTAAAG TTAATGCATT AAGAAGAGAT TAGATAGGGA TGGTGGCGTA TCTTCCTACA 600
GTTTCCTGT TAACAAGAAA GTCAGAGGTC AGTTGATCAG ACATTAGATT ATTTATTGCT 660
45 AAAACTAAAA AAAATTAAAA AAACTGGAG GGGGGCC 697

50

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

60 CGTGAGTCAC CTCTCTATAG TGGGCGTGGC CGAGGCCGGG GTGACCCTGC CGAAGCCTCC 60

GCTGCCAGAA ACCATGTTCA AGGTAATTAA AAGGTCCGTG GGGCCAGCCA GCCTGAGCTT 120
 GCTCACCTTC AAAGTCTATG CAGCACCAAA AAAGGACTCA CCTCCCAAAA ATTCCGTGAA 180
 5 GGTGTATGAG CTTTCACTCT ACTCAGTTCC TGAGGGTCAA TCGAAGTATG TGGAGGAGGC 240
 AAGGAGCCAG CTTGAAGAAA GCATCTCACA GCTCCGACAC TATTGCGAGC CATAACAAC 300
 10 CTGGTGTGAG GAAACGTA CTCCAACTAA GCCCAAGATG CAAAGTTTGG TTCAATGGGG 360
 GTTAGACAGC TATGACTATC TCCAAAATGC ACCTCCTGGA TTTTTCCTGA GACTTGGTGT 420
 TATTGGTTT GCTGGCCTTA TTGGACTCCT TTGGCTAGA GGTTCAAAA TAAAGAAGCT 480
 15 AGTGTATCCG CCTGGTTTCA TGGGATTAGC TGCCTCCCTC TATTATCCAC AACAAGCCAT 540
 CGTGTTTGCC CAGGTCAGTG GGGAGAGATT ATATGACTGG GGTTCACGAG GATATATAGT 600
 20 CATAGAAGAT TTGTGGAAGG AGAAGTTTCA AAAGCCAGGA AATGTGAAGA ATTCACCTGG 660
 AACTAAGTAG AAACTYCAT GTCTGCCAT CTTAATCAGT TATRGGTAAA CATTTGGAAC 720
 TCCATAGAAT AAATCAGTAT TTCTACAGAA AAATGGCATA GAAGTCAGTA TTGAATGTAT 780
 25 TAAATGGCT TTCTTCTTCA GGAAAACTA GACCAGACCT CTGTTATCTT CTGTGAAATC 840
 ATCCTACAAG CAACTAACC TGAATCCCT TCACCTAGAG ATAATGTACA AGCCTTAGAA 900
 30 CTCTCATTC TCATGTTGCT ATTTATGTAC CT 932

35 (2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 661 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

45 GTCATTCTTT AAATAAAGC TTCTCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA 60
 AGATTCCCC TAGGGTTGAT ATGTGTCTAA TTCATTTTAT AAAAATTATT CTTGTCTTCA 120
 TTTTAAAGCT TTGGCTATAT AGTCAGAAAT GTCCTAAATA ACAAACTATT TTGTATTTAA 180
 50 TTTAGGGAAG ACTAAAGGA AGAAAAATGA AAAGTCAGTC TTTATGTAAG CTCCAAGGAT 240
 ATTAGGGCTT AAAGGGCTTT TCTAGTTTTA TGAGAATTG TACTACTGAT TTTTATATAT 300
 55 TCCTGTTTTT GAGATGAACA GATCTCTGGG GAAATGTTG AGTTACAATG GCATTTCACT 360
 GTGATCCCTC TCAAGCTCAG ATCAGTTCTA TAACCAATG ACAACCTGTC TCTTTGGTTT 420
 ACTGTCTGT GAAATGTCAG CTCAAGTTTC CCAGAAGTCG TGTGTTTATG ATGAGTCAGA 480
 60

GTGCTTTTCC TCGGTGGGAC AGTTGCTGGC CCTCTTAATT TTGGTGTATG TGCTTCCAAG 540
TATCTAAACC TCAGTCTGA TCTGTATATG CTATCCTAAC TGTTAATTGT ATTATTGATT 600
5 ATGTTGATTA TCTTGCTTGA AGGTTTCATAC TTTTCAATTG GATAGAAATA AAGTTTTTTT 660
C 661

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(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GAAACTGACA TTGTTAAACA CACTAAAACA GAAGTACTTA CCTCTTGAAG ATTTAATATA 60
TAATGGTTGA CATGATACAT GTACATGAAT GGAATGACCA GATGCTTATG GTCTACATTT 120
25 TCCTTTATCC TGTAGTATT ACCTTCCTTA ATCTTTGTTC CTTAACATGC TAAATTCCTC 180
TTCAGTGTTC ATTTTCTAGT GACAGAATGC TAACATTTCT TACACCCTGG CAGAAGGGAG 240
30 AGAAATGTGT TTTGGGGTGG GTAACAAAT TTTTGAGTGA AATATCATAA GATGAGAATG 300
GAAAGAGGGA GACACAAAGA GTTATAACAA AAAACAATG GTTTTTTTAG CCATTGACT 360
GGCTCTTTAA ATAGTCTACA AGACATTCAC GTTNAACATC ACTTTTAGTG AAATAAAATG 420
35 TGCCATACTA GTATGTGCTT CAAAAGGGCA AATGTGCTTT AGTGCCCTAA GGCTAAATTT 480
TGTCATTTG ACATCAGAGA TGTTGTAAGT ATTGCACITA ATACGCACCT ATTTCTCAAT 540
40 AGTGNATTTT TTTTGGCTAG CATTTNCTTT ACCACTAACC TTGTTGGATA GC 592

45 (2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 938 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

55 TGGAGTGGCT TTCCAGCTGA ATGAATCCTA TGCTCGCGT GCAGGTGGTT GGTTTTCAAT 60
GTTCTTSCTA ATTTTTTTCC TATTGGCTCT TGGGAGTTN CTTTGTTC TCCTGTGTTT 120
GCCCAGCTTT AATAAAACCA GCGCAAACA AAAACCATAG CATTCTGAAA CAATAGGGGG 180
60

CCCACATGG ACCCAGTATG TCACTTTAAT GGAATTCAAG AAAAAATCTG AATGGGAAAA 240
TGACACTAGG AATGTATACT CCACACATTT TATGCCATAT AATGGTGTGT TTTCTTAATT 300
5 TTGTTTCTTG TGGCGAAATG TGGCTTTCAA ATTAAAAATGM CCTTTTCTTC TTKGAAACTT 360
TTTGTMTKGA CTKGTATAAT TAAGGGTTTG GAAAGATTCA TAATMTGAG AGAGGTTTGC 420
AACCAGGAGA TACAAAGAAG TCTCAGTAGT AATCTTGTTT ATGTGCTTTT ACAGCCAGCT 480
10 ACATTTAAGR ATGTATTAGT TACAGAAATT ATATGTCTGT GTATGTGTCT CTAACAATA 540
AAGTACATGC CTCCACATAA TGGGTGCTG TCCATCTCGG CAAATACTGG CCAAGTCCCT 600
15 TTATGACAGG CACACAGAAA CCATAGCATG GTCTGGCTTT CAGAAAATGC CTCTCATCTT 660
TCCTGGAACC TTATTTTGCT AAATGTCTGT TTTCTTGTA TTTGTGTAC CTCACAGCAC 720
CATTGTGACC ATGGTGATGC CTCATTTGCA TGATATGTAC CTTGTGTTTA ATGTGAAATA 780
20 CATTTTCATT GAAGAGTCTG ATGACTTGCT AGCGTTTAT TTTTCTGTA AGCTCAATGT 840
GCTGAAACCA AACCAGGCTT TAAAAACCT GTGTAGAAGA AAACCAAAAA ATCCTGTGTG 900
25 GGTGTCCTTT CCCTGTCAA CTCAATAAAA ATTCCTTT 938

30 (2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1079 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

40 AGCCTGCCGG GAGAGTGGTG GCATCTRARA GGCTGGTCTG GACTGTGGT TGGGGAGGT 60
GGGAGCTGTT TTAACCGTGT GCGGCTCTC CTGTGCKGC GTGGGCATCC CCGGGGCAG 120
TGAACGCGG GCGCTCCTCC AGCTTCCGAG TCCAGCCAGC CTGGGCGCGG GCGCGCCCC 180
45 CGAGACACCC GAGGAGTCCG TTCTCCCTG GTTACGTGA CTGTGGAGCT GGTCTCTGT 240
GGCTCAGCGC CGTGCGGAGG TTGAAGCGTA CCTGCGGAGC TCGCACCAGG GCGGTGAGGA 300
GGAGGAGGAA GGGCATGAGC CGAGCTGAG GAATCCGTGY TCCAACTCT AACTCAAGG 360
RTGCMCTCG CAACTCTGGT GCGATGGGC TGGGGCAGAT GTCTTGGAG TTCTACCAGA 420
AGAAGAAGTC TCGCTGGCCA TTCTCAGAC AGTGCAATCC ATGGGAAGTG TGGACGGTCA 480
55 AGGTGCATGT GGTAGCCCTG GCCACGGAGC AGGAGCGCA GATCTGCCG GAGAAGGTGG 540
GTGAGAACT CTGCGAGAAG ATCATCAACA TCGTGAGGT GATGAATCG CATGAGTACT 600
60 TGCCAAGAT GCCACACAG TCGGAGGTG ATAACGTGTT TGACACAGG TTGCGGGAGC 660

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TGCAGCCCTA CCTGTACAAG ATCTCCTTCC AGATCACTGA TGCCCTGGGC ACCTCAGTCA 720
CCACCACCAT GCGCAGGCTC ATCAAAGACA CCCTTGCCCT CTGAGCGTCG CTGGATCTCT 780
GGGAGCTCCT TGATGGCTCC CAGACCTTGG CTTTTGGGAA TTGCACTTTT GGGCCTTTGG 840
GCTCTGGAAC CTGCTCTGGG TCATTGGTGA GACTTGGAAG GGGCAGCCCC CGCTGGCTTC 900
TTGGTTTGT GGTGGCCAGC CTCAGGTCAT CCTTTTAATC TTTGCTGACG GTTCAGTCCT 960
GCCTCTACTG TCTCTCCATA GCCCTGGTGG GGTCCTCCCTT CTTTCTCCAC TGTACAGAAG 1020
AGCCACCACT GGGATGGGGA ATAAAGTTGA GAACATGAGT TTGGGCTGAA AAAAAAAAAA 1079

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

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TGAAGCAGGC GCTCTTGGCT CGGCGCGGCC CGTGCAATC CGTGGAGGAA CGCGCCGCCG 60
AGCCACCATC ATGCTTGGGC ACTTACAGGA AGGCTTCGGC TGCCTGGTCA CCAACCGATT 120
CGACCAGTTA TTTGACGACG AATCGGACCC CTTGAGGTG CTGAAGGCAG CAGAGAACAA 180
GAAAAAAGAA GCCGGCGGGG GCGCGTTGG GGGCCCTGGG GCCAAGAGCG CATCAGGGCC 240
GCGGCCCAGA CCAACTCCAA CGCGGCAGGC AAACAGCTGC GCAAGGAGTC CCAGAAAGAC 300
CGCAAGAACC CGCTGCCCCC CAGCGTTGGC GTGGTTGACA AGAAAGAGGA GACGCAGCCG 360
CCCGTGGCGC TTAAAGAAAG AAGGAATAAG ACGAGTTGGA AGAAGACCTG ATCAACAACT 420
TCAGGGTGAA GGGAAAATAA TTGATAGAAG ACCAGAAAGG CGACCACCTC GTGAACGAAG 480
ATTTCGAAAAG CCACTTGAAG AAAAGGGTGA AGGAGGCGAA TTTTCAGTTG ATAGACCGAT 540
TATTGACCGA CCTATTGAG GTCGTGGTGG TCTTGAAGA GGTGAGGGG GCCGTGGACG 600
TGGAATGGGC CGAGGAGATG GATTTGATTG TCGTGGCAA CGTGAATTTG ATAGGCATAG 660
TGGAAGTGAT AGATCTTCTT TTTACATTA CAGTGGCCTG AAGCACGAGG ACAAACGTGG 720
AGGTAGCGGA TCTCACAAC TGGGAACCTGT CAAAGACGAA TTAAC TGACT TGGATCAATC 780
AAATGTGACT GAGGAAACAC CTGAAGGTGA AGAACATCAT CCAAGTGGCAG AACTGAAAA 840
TAAGGAGAAT GAAGTTGAAG AGGTAAAGA GGAGGTCCA AAAGAGATGA CTTTGATGA 900
GTGAAGGCT ATTCAAAATA AGGACCGGC AAAAGTAGAA TTTAATATCC GAAACCAAA 960

	TGAAGTGTCT GATGGGCGCT GGAAGAAGGG ATTTGTCTTT CATAAATCAA AGAGTGAAGA	1020
	GGCTCATGCT GAAGATTCGG TTATGGACCA TCATTTCGGG AAGCCAGCAA ATGATATAAC	1080
5	GTCTCAGCTG GAGATCAATT TTGGAGACCT TGGCCGCCCA GGACGTGGCG GCAGGGGAGG	1140
	ACGAGGTGGA CGTGGGCGTG GTGGGCGCCC AAACCGTGGC AGCAGGACCG ACAAGTCAAG	1200
	TGCTTCTGCT CCTGATGTGG ATGACCCAGA GGCATTCCCA GCTCTGGCTT AACTGGATGC	1260
10	CATAAGACAA CCCTGGTTCC TTTGTGAACC CTCTGTTC AAGCTTTTGC ATGCTTAAGG	1320
	ATTCCAAACG ACTAAGAAAT TAAAAAATAA AAGACTGTCA TTCATACCAT TCACACCTAA	1380
15	AGACTGAATT TTATCTGTTT TAAAAATGAA CTCTCCCGC TACACAGAAG TAACAAATAT	1440
	GGTAGTCAGT TTTGTATTTA GAAATGTATT GGTAGCAGG ATGTTTTCAT AATTTTCAGA	1500
	GATTATGCAT TCTTCATGAA TACTTTTGTA TTGCTGCTTG CAAATATGCA TTTCCAAACT	1560
20	TGAAATATAG GTGTGAACAG TGTGTACCAG TTAAAGCTT TCACTTCATT TGTGTTTTTT	1620
	AATTAAGGAT TTAGAAGTTC CCCCAATTAC AAACGTGTTT TAAATATTGG ACATACTGGT	1680
25	TTTAATACCT GCTTTGCATA TTCACACATG GTCAACTGGG ACATGTTAAA CTTTGATTTG	1740
	TCAAATTTTA TGCTGTGTGG AATACTAACT ATATGTATTT TAACTTAGTT TTAATATTTT	1800
	CATTTTTGGG GAAAAATCTT TTTTCACTTC TCATGATACC TGTTATATAT ATATGCTAAA	1860
30	TCTTTATATA CAGAAATATC AGTACTTGAA CAAATTCAAA GCACATTTGG TTTATTAAAC	1920
	CTTGCTCCTT GCATGGCTCA TTAGGTTCAA ATTATAACTG ATTTACATTT TCAGCTATAT	1980
35	TTACTTTTTA AATGCTTGAG TTTCCCATTT TAAATCTAA ACTAGACATC TTAATTGGTG	2040
	AAAGTGTMTT AAACACTTAA TTGTTGGTAG GCACATCGTG TCAAGTGAAG TAGTTTTATA	2100
	GGTATGGGTT TTTTCTCCCC CTTCAACAGG GTGGGTGGAA TAAGTTGATT TGGCCAATGT	2160
40	GTAATATTTA AACTGTTCTG TAAATAAGT GTCTGGCCAT TTGGTATGAT TTCTGTGTGT	2220
	GAAAGTCCC AAAATCAAAA TGGTACATCC ATAATCAGCC ACCATTTAAC CCTTCTTGT	2280
45	TCTAAAACAA AAACCAAAGG GCGCTGGTTG GTAGGGTGAG GTGGGGGAGT ATTTTAATTT	2340
	TTGGAATTTG GGAAGCAGAC AGCTTTACTT TGTAAGGTTG GAACAGCAGC ACTATACATG	2400
	AAATATAAAC CAAAAACCTT TACTGTTTCT AAATTTCTTA GATTGCTATT ATTTGGTTGT	2460
50	AAGTTGAGTA TTCCACAGAA AGTGGTAATT ATCTCTTCTC TCTTCTCCA TTAGAAAATT	2520
	AGGTAAATAA TGGATTCTTA TAATGGGAGC ATCACCCTT ATTAACAC ACATAGAATG	2580
55	ATGAATTAAA AAAGTTTCT AGGATTGTCT TTTATTCTGC CACATTTATT GATAAACAGT	2640
	GAAGGAATTT TTAATAAATT TTAAGAAAT GTTTGTACAG TCATTTTAG AAATGTTCTA	2700
60	CCTGTATATG GTAATGTCCA GTTTTAAAAA TATTGGACAT CTCAATCTT AAACATTTCT	2760

ATTTAGCTGA TTGGTCTCA CATATACTTC TAAAAGAAAC TTTTATGTTA TAAGAGTTAC 2820
 TTTTGGATA AGATTATTA ATCTCAGTTA CCTACTATTC TGACATTTTA GGAAGGAGGT 2880
 5 AATTGTTTTT AATGATGGAT AAACCTGTGC TGGTGTMTTG GATCTTATGA TGCTGAGCAT 2940
 GTTCTGCACT GGTGCTAATG TCTAATATAA TTTTATATTT ACACACATAC GTGCTACCCA 3000
 GAGATTAATT TAGTCCATAT GAACTATTGA CCCATTGTTC ATTGAGACAG CAACATACGC 3060
 10 ACTCCTAAAT CAGTGTGTTT AGACTTTTCA AGTATCTAAC TCATTTCCTAA ACATGTACCA 3120
 TGTMTTATAA ACCTCTTGAT TTCCAGCAAC ATACTATAGA AAACACCTGC TACTCAAAAC 3180
 15 ACAACTTCTC AGTGTCTATCC ATTGCTGTCTG TGAGAGACAA CATAGCAATA TCTGGTATGT 3240
 TGCAAGCTTT CAAGATAGCC TGAACCTAAA AAGTGGTGC ATTAGTTGTA TCTGATGGAT 3300
 ATAAATTTGC CTCCTAGTTC ACTTTGTGTC AAGAGCTAAA ACTGTGAACC TAACTTTCTC 3360
 20 TTATTGGTGG GTAATAACTG AAAATAAAGA TTTATTTTCA TGCTCACTTC TTTAAAGTCA 3420
 TAAAAACAAT CAAATAGGRT CATGTTTATT GTCATGTGTT TCCTGGKTTT TGACCTGTGT 3480
 25 GCACACCCCT GTGTGTTTAT AATTTTTTAAA TTGAATTTTA TATGGGGTTT TTATTTGCTA 3540
 AAAACCAGGC TGTGAATCA CATTTGGGAA GGGTACTTAT CTTAATGACT AATGACTTAA 3600
 TTGGGAAAGT TGAATTTCTG TAAAATACAA AATCCAAGGA CTTCTTGGGA TTTAATCTAA 3660
 30 TTGTCACTTC NITAGGCAGA TNCACCTTTT TGGATAATGG AAAGTTAAGC ATACCGAATG 3720
 CTACTTTTGG TTGACAAACG GGCCTAATAG TCCGGGGGA AATCCCTAAC NGGTAAGGNT 3780
 35 CCCAAGTATG G 3791

40 (2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1334 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

50 CAGTGCTCGC TCCTGCTCGG GCGCTGCGG CCCCAGGCGT CGCCATGACC AGTGAGCTGG 60
 ACATCTTCGT GGGGAACAGA CCCTTATCGA CGAGGACGTG TATCGCCTCT GGCTCGATGG 120
 TTA CTGCTG ACCGACGCGG TGGCCCTGCG GGTGCGCTCG GGAATCCTGG AGCAGACTGG 180
 55 CGCCACGGCA GCGGTGCTNC AGAGCGACAC CATGGACCAT TACCGCACCT TCCACATGCT 240
 CGAGCGGCTG CTGCATGCGC CGCCCAAGCT ACTGCACCAG YTCATCTTCC AGATTCCGCC 300
 60 CTCCCGGCAG GCACTACTCA TCGAGAGGTA CTATGCCTTT RATGAGGCCT TTGTTCCGGA 360

5 GGTGCTGGGC AAGAAGCTGT CCAAAGGCAC CAAGAAAGAC CTGGATGACA TCAGCACCAA 420
 AACAGGCATC ACCCTCAAGA GCTGCCGGAG ACAGTTTGAC AACTTTAAAC GGGTCTTCAA 480
 GGTGGTAGAG GAAATGCGGG GCTCCCTGGT GGACAATATT CAGCAACACT TCCTCCTCTC 540
 TGACCGGTG GCCAGGGACT ATGCAGCCAT CGTCTTCTTT GCTAACACC GCTTTGAGAC 600
 10 AGGGAAGAAA AACTGCAGT ATCTGAGCTT CGGTGACTTT GCCTTCTGCG CTGAGCTCAT 660
 GATCCAAAAC TGGACCTTG GAGCCGTCGA CTCACAGATG GATGACATGG ACATGGACTT 720
 AGACAAGGAA TTTCTCCAGG ACTTGAAGGA GCTCAAGGTG CTAGTGGCTG ACAAGGACCT 780
 15 TCTGGACCTG CACAAGAGCC TGGTGTGCAC TGCTCTCCGG GGAAAGCTGG GCGTCTTCTC 840
 TGAGATGGAA GCCAACTTCA AGAACCTGTC CCGGGGGCTG GTGAACGTGG CCGCCAAGCT 900
 20 GACCCACAAT AAAGATGTCA GAGACCTGTT TGTGGACCTC GTGGAGAAGT TTGTGGAACC 960
 CTGCCGCTCC GACCACTGGC CACTCAGCGA CGTGCGGTTT TTCCTGAATC AGTATTCAGC 1020
 GTCTGTCCAC TCCTCGATG GCTTCCGACA CCAGGCCTCT GGGACCGCTA CATGGGCACC 1080
 25 CTCCGCGGCT GCCTCCTGCG CCTGTATCAT GACTGAGGTG CCTCCCAACG CTCCGCCAC 1140
 GCTGACAATA AAGTTGCTCT GAGTTTGGAG ACTGGTCTC GCTCCGGGGA GCAAGTGGG 1200
 30 GCGGTGCAGA TGTGCTGTG TCTGTCTCTG AGCACCTGGT GTCCGTGTAC AAGGATGGAT 1260
 GTGTNCNGTG GCTCCTTGGG AACTGAGACA TATCTCAGG AATGGTGTCT GTGCTCAGCC 1320
 CATCCACCAG AAGA 1334
 35

(2) INFORMATION FOR SEQ ID NO: 216:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

50 GTGGCGGGGA TGCTGCGAGG GGTCTCCTG CCCCAGGCG GCCGGCTGCC TACCCTCCAG 60
 ACTGTCCGCT ATGGCTCCAA GGCTGTTACC CGCCACGTC GTGTGATGCA CTTTCAGCG 120
 CAGAAGCTGA TGGCTGTGAC TGAATATATC CCCCCGAAAC CAGCCATCCA CCCATCATGC 180
 55 CTGCCATCTC CTCCAGCCC CCCACAGGAG GAGATAGGCC TCATCAGGCT TCTCCGCCGG 240
 GAGATAGCAG CAGTTTCCA GGACAACCGA ATGATAGCCG TCTGCCAGAA TGTGGCTCTG 300
 AGTGCAGAGG ACAAGCTTCT TATGCGACAC CAGCTGCGGA AACACAAGAT CCTGATGAAG 360
 60

	RTCTTCCCA ACCAGGTCCT GAAGCCCTTC CTGGAGGATT CCAAGTACCA AAATCTGCTG	420
	CCCCTTTTTG TGGGGCACAA CATGCTGCTG GTCAGTGAAG AGCCCAAGGT CAAGGAGATG	480
5	GTACGGATCT TAAGGACTGT GCCATTCTTG CCGCTGCTAG GTGGCTGCAT TGATGACACC	540
	ATCCTCAGCA GGCAGGGCTT TATCAACTAC TCCAAGCTCC CCAGCCTGCC CCTGGTGCAG	600
	GGGGAGCTTG TAGGAGGCCT CACCTGCCTC ACAGCCCAGA CCCACTCCCT GCTCCAGCAC	660
10	CAGCCCCTCC AGCTGACCAC CCTGTTGGAC CAGTACATCA GAGAGCAACG CGAGAAGGAT	720
	TCTGTCATGT CGGCCAATGG GAAGCCAGAT CCTGACACTG TTCCGGACTC GTAGCCAGCC	780
15	TGTTTAGCCA GCCCTGCGCA TAAATACACT CTGCGTTATT GGCTGTGCTC TCCTCAATGG	840
	GACATGTGGA AGAACTTGGG GTCGGGGAGT GTGTTTGTC CTTGGTTTTT ACTAGTAATG	900
	ATATTGTCAG GTATAGGGCC ACTTGAGAT GCAGAGGATT CCATTTCAGA TGTCAAGTAC	960
20	CGGCTTCGTC CTTAGTTTTT CCAACTTGGG ACGTGATAGG AGCAAAGTCT CTCCATTCTC	1020
	CAGGTCCAAG GCAGAGATCC TGAAAAGATA GGGCTATGTG CCCCTGCCTC CTTGGTCACT	1080
25	GCCTCTTGCT GCACGGGCTC CTGAGCCACC CCCTTGGGGC ACAACCTGCC ACTGCCACAG	1140
	TAGCTCAACC AAGCAGTTGT GCTGAGAATG GCACCTGGTG AGAGCCTGCT GTGTGCCAGG	1200
	CTTTGTGCTG AGTGCTGTAC ATGTATTAGT TCCTTTACTG CTGACCACAT TGTACCAATT	1260
30	TCACAGAGAA GGAGCAGAGA AATTAAGTGG CTTGCTCAAG GTCATGCAGT TAGTAAGTGG	1320
	CAGAACAGGG ACTTGAACCA AGCCCTCTGC TCTGAAGACC GCGTCCTGAA TTTCTTCACT	1380
35	AGAGCTTCCT CATCAGGTTA CCCAGAAGTG GGTCCCATCC ACCATCCAGG TGTGCTTGGA	1440
	TGTTAGTTCT CCACCCTCGA GGTGTACGCT GTGAAAAGTT TGGGAGCACT GCTTTATAAT	1500
40	AAAATGAAAT A	1511

(2) INFORMATION FOR SEQ ID NO: 217:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

	AGGCCTTACT TTTCTCCCA CAAAGGAGTC GCAGCCACGC TAGCTCTGAC TTGCCACTGT	60
55	GACAAAGTTC ACGTAGCAGG TCTAGGCAAA GACTGGGCAA TTGAGCAGAG GAGACGGACC	120
	TGTGAGTCTG ACCRYGAGSC GGRCCCTTC ACCTTGGCTG GGCTGGTCCT GGTCCCTAGG	180
60	TTTGTGTCAGG TTGTCCTTGT TTGGATCCCT CAACTAGGTG ATAAGCACTG GAGGGGGATG	240

ACCCGCCTTG GACGTGTTTC TTAACTCA TCCATATAAT AGGGCCGTGG GATGGTTGTA 300
GAGGTAAAGC AGGATGATGG TGTTTTAAGA CCAGAGCTTG GGACCAGGGC TCCTACACCT 360
5 AATTTTCTCT CCTGGTAGCT GAACAAAGGT CTAAATTAGC TTAACAAAAG AACAGGCTGC 420
CGTCAGCCAG AGTTCTGAAG GCCATGCTTT CAGTTTCCCT TGTGACAAT TGCTCTCCAG 480
10 TTCTATGAA AGCACAGAGC CTTAGGGGGC CTGGCCACAG AACACAACCA TCTTAGGCCT 540
GAGCTGTGAA CAGCAGGGGG TTGTGTGTCT GTTCTGTTTC TCTGCTTGCC GAACTTTCTC 600
AATAAACCTT ATTTCTTATT TTATATTAC GTNGTGCTG GG 642
15

(2) INFORMATION FOR SEQ ID NO: 218:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

GGTCCCACTG TTCCATTITA TGCTAATAGA TTCCATTCTA GGGCCCAGCC GTCTCTTGAC 60
30 TGATGGTGTG CCGTTTAACC CTTGGCATGT ATAATAGAAT TTTGGTGAAT GAAAGAACCC 120
AAATAGGCCA GATAGTCCCC CCAGGCCCTG ATATCCATAA AAGGCTGGG AATGCATTAT 180
35 GTAATTGTCC TTAGTCTTTT TGTGTGTTTA GAAAAAAAAA ACAAGATGGG CTCAGATGGA 240
TGCCTACGTA AAAATGGTTC CTAGCTGTGT ACTCATAACT TTTCTTTGAA TTGAGTAGTG 300
AAAGGAAGGA GGAGGAAAGG AAATTAAATG TCCTTCTAGT ATTCTCTGGA CTCAAGTCTG 360
40 ACATATGRGA TAATAACCTA TATTGAAATG CCAAGAATTG TATCTGAAAC AAGRGACAG 420
TTTGACACAT TTATCATGCC TTCATATTAC ATATTAACTG AAACCAATTA ATAAACATAT 480
45 GAAATATCCA TGGCACAAGG CAAAGGCACC TAAACCTTTT GTTCTTTTTT CTACATAGCA 540
GAAATTGATT TTTTTTTTAT TTTTTTAGGG GAACCTATAT AATTATGACC CAGTGATGTC 600
TTTTGGTGAC TTAAGCTTAT GAATTCAGGT TACAATTGAG TTGATCTAG ATGGTTACTA 660
50 CCTTGAAAAG GATGTTGGTG CCTTATGTGA CAGGAGCCAG AGCCTGCTGG GAATAACAA 720
AGCAGATTCA TGCCAACACC AACTCGTAGC TTTAGTGCCA GATGGGAGTG GTCACAGACT 780
55 CCCAAAATGT GGGGCTTTGG ATTTCCACAC CATCCACGT GTGTGTCATC TTCTCTTTTC 840
ACACTCTTGA TGATAATTG AAAATGRTGA AATCACCTCT GAATTTGCCT ATAGCATGAG 900
CACATTCTTA TGACAACATA ACAAATAGTT CATAATGTGA ATATTAGAAA CTGTTACAGC 960
60

CTGCAGTAC CATAATTTTC CATGTTTGTG GAATTGATAT TGAAATAGCA GGGCTAAGGA 1020
ATTACTGGCA AGTTTTAGCC TGTGGTAAT ACCTTAGGGT TATTTAAATA TTTGTAATTT 1080
5 TATTTAAATG TTCATGAATG TTTGAAAGGA ACAAATTAT CAGGGATGGC TCTTTGCCAT 1140
GGGTCTTATT TTCACCTCT TTTCTGTAAG AAAAAAGAAC AATGTCTTAA TGTATTTTAA 1200
AAGTTTTTGG TATAGTTTCT AATTCCAATT TTAATAAAG T 1241
10

(2) INFORMATION FOR SEQ ID NO: 219:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

20

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

TGTTTATGTG ACCTAAAACA TACACACATG CACACACACA TACATATCCA TTCATTCATT 60
25 CATTCAAGTG GTGTTCCAG TGCTGTGTG TCACTGTTTA TGCAGTTTCC ATTTCCCACT 120
GAATTATGAG TGGAGGGCAA CTTTCTAAC CAGATTGTCT TTTCAGAACA AAGACCKGGG 180
30 RATGAGGAA GAGTTTGAA AGAGGGAGAG GCAAGGAAAG AGAGCTTTAA ATGAAAGGT 240
TAATTTCTTA AGAGGAACCT GGGCTGAATG ACTACAGTGT TATACCTCC AATCTTTGCA 300
GGTGGGCATG GAACACTGCT TGTATCACTC TGTGCACGGT ATAAATCCAT ATATCCACAA 360
35 AAACACACAT CCATCCATCA ACATATACAT GGTTTGGGAT GAGCAGGTCA ATAGTTTGA 420
GAGGGAGTTT GTTCTTTTT TTTCTCATT ATACTCTTAA ATGTGTGCA GTTATCAAAC 480
40 AAACAAACAG AAAAATGTT TGGGAAAAAC CTGTCATACG CCTTTCTAT CMAGTGCTTT 540
AAAATATAGA CTAAATACAC ACATCCTGCC AGTTTTTCT TACAGTGACA GTATCCTTAC 600
CTGCCATTTA ATATTAGCCT CGTATTTTT TCACGTATAT TTACCTGTGA CTTGTATTTG 660
45 TTATTTAAAC ACGAAAAAA ACATTCAAAA AAAGAAAAAT TAACTGTAGC GCTTCATTAT 720
ACTATTATAT TATTATTATT ATTGTGACAT TTTGGAATAC TGTGAAGTTT TATCTCTTGC 780
ATATACTTTA TACGGAAGTA TTACGCCTTA AAAATACGAA AATAAATTTT ACAAGGTTTC 840
TGTTTTGTGT GGAAGAGTAA TTCATGTTGC TAAGAATGAT GTTTGTTTTT TTGGGGTTTT 900
TGTGTTTTTT TTTTAAATG TTACCAGCAC TTTTTTGTGA AGTTTCACTT TCCGAGGTAT 960
55 TGTACAAGTT CACACTGTTT GTGAAGTTG AATATGAAGG AATAATTAAA AAAAAAAAAA 1020
AAACCNCGGG GGGGGCCCCG TCCCATTGGN CCAAGGGGG CGGTACGGG GTCACGGCCG 1080
60

(2) INFORMATION FOR SEQ ID NO: 220:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TGAATTGAGG GCTTAAAGAT AACATATGG GRTTGGAGTT GTGTGTCCAT AGGGTTTCAC 60
TGCCTATTGT ATTTGAGTTT ATCCCTATTA ATTTTTTACA GTGAAATTTT ATTAAAGTAT 120
AATGTACATA TATTTTCAGT GGATTTTGCT CTGAAGGTC TCCAGTGGTC TGA CTACGAG 180
ATAGTGCGGC TTCAGCTGTG GGATATTGCA GGGCAGGAGC GCTTCACCTC TATGACACGA 240
TTGTATTATC GGGATGCCCTC TGCCTGTGTT ATTATGTTTG ACGTTACCAA TGCCACTACC 300
TTCAGCAACA GCCAGAGGTG GAAACAGGAC CTAGACAGCA AGCTCACACT ACCCAATGGA 360
GAGCCCGTGC CCTGCCTGCT CTTGGCCAAC AAGTGTGATC TGTCCCCTTG GGCAGTGAGC 420
CGGGASCAGA TTGACCGGTT CAGTAAAGAG AACGGTTTCA CAGGTTGGAC AGAAACATCA 480
GTCAAGGAGA ACAAAAATAT TAATGAGGCT ATGAGAGTCC TCATTGAAAA GATGATGAGA 540
AATTCACAG AAGATATCAT GTCTTTGTCC ACCCAAGGGG ACTACATCAA TCTACAAACC 600
AAGTCTCCA GCTGGTCTG CTGCTAGTAG TGTTTGGYTT ATTTTCCATC CCAGTTCTGG 660
GAGGTCTTTT AAGTCTCTTC CCTTTGGTTG CCCACCTGAC MATTTTATTA AGTACATTTG 720
AATGTCTCC TGA CTACTGT CCAGTAAGGA GGCCCATTTG CACTTAGAAA AGACACCTGG 780
AACCCAKGTG CATTTCTGCA TCTCTGGAT TAGCCTTTSA CATGTTGCTG RCTCACATTA 840
GTGCCAGTGA GTGCCTTCGG TGTAAGATCT TCTCATCAGC CCTCAATTTG TGATCCGGAA 900
TTTTGTGAGA AGGATKAGAA ATCAGCACCT GCGTTT TAGA GATCATAATT CTCACCTACT 960
TCTGAGCITA TTTTCCATT TGATATTCAT TGATATCATG ACTTCCAATT GAGAGGAAAA 1020
TGAGATCAAA TGTCAATTC CAAATTTCTT GTAGGCCGTT GTTTCAGATT CTTTCTGTCT 1080
TGGAATGTAA ACATCTGATT CTGGAATGCA GAAGAGGGG TCTGGGCATC TGTGGATTTT 1140
TGGCTACTAG AAGTGTCCTA GAAGTCACTG TATTTTGTAA ACTTCTAACG TCATAATTAA 1200
GTTTCTCTTG TCTTGGGCAT CAAGANTAGT TCCAATTTT TGGGCCGGG CAGGGTGG 1258

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(2) INFORMATION FOR SEQ ID NO: 221:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

	CACAATATAT GAAATAGTAC CCTCTAAAAA AGAGAAAAAA AAAATCAGGC GGTCAAACCTT	60
10	AGAGCAACAT TGTCTTATTA AAGCATAGTT TATTTCACTA GAAAAAATTT AATATCAAGG	120
	ACTATTACAT ACTTCATTAC TAGGAAGTTC TTTTAAAAAT GACACTTAAA ACAATCACTG	180
	AAAACCTGAT CCACATCACA CCCTGTTTAT TTTCTTAAA CATCTTGGA GCCTAAGCTT	240
15	CTGAGAATCA TGTGGCAAGT GTGATGGGCA GTAAAATACC AGAGAAGATG TTTAGTAGCA	300
	ATTAAAGGCT GTTGCACCT TTAAGGACCA GCTGGGCTGT AGTGATTCTT GGGGCCAGAG	360
20	TGGCATTATG TTTTACAAA ATAATGACAT ATGTCACATG TTTGCATGTT TGTTCCTTG	420
	TTGAATTTTT GAACAGCCAG TTGACCAATC ATAGAAAGTA TTACTTTCTT TCATATGGTT	480
	TTTGGTTCAC TGGCTAAGA GGTTCCTCAG AATATCTATG GCCACAGCAG CATACCAGTT	540
25	TCCATCCTAA TAGGAATGAA ATTAATTTTG TATCTACTGA TAACAGAATC TGGGTCACAT	600
	GAAAAAAT CATTTTATCC GTCTTTAAG TATATGTTA AAATAATAAT TTATGTGTCT	660
30	GCATATTGCA GAACAGCTCT GAGAGCAACA GTTCCCATT AACTCTTCT GACCAATAGT	720
	GCTGGCACCG TTGCTTCCTC TTTGGAAGA GGAAAGGTG TGTGAACATG GCTAACCAATC	780
	TTCAAATACC CAAATTGTGA TAGCATAAAT AAAGTATTTA TTTTATGCCT CAGTATATTA	840
35	TTATTTAATT TTTAGGTAA TGCCTATCTC TTGGTCTATT AAGGAAAGAA GCAATCAGTA	900
	GAGAATTCAG GATAGTTTG TTTAAATTCT TGCAGATTAC ATGTTTAC AGTGGCCTGC	960
40	TATTGAGGAA AGGTATTCTT CYATACAACT TGTTTTAACC TTTGAGAACA TTGACAGAAA	1020
	TTATGCAATG GTTGTGAG ATACGGACTT GATGGTCTG TTTAATCAGT TTGCTTCCAA	1080
	AGTGGCTAC TCAAGAGGCC CTAAGACTGG TAGAAATTAA AAGGATTTCA AAAACTTTCT	1140
45	ATTCTTTCT TAAACCTACC AGCAAACCTAG GATTGTGATA GCAATGAATG GTATGATGAA	1200
	GAAAGTTGA CCAAATTTCT TTTTGTGTTG TTGTTGTTGT TTTGAATTTG AAATCATTCT	1260
50	TATTCCTTTT AAGATGTTT ATGTATGAGT GTGAAGATGC TAGCGAACCT ATGCTCAGAT	1320
	ATTCATCGTA AGTCTCCCTT CACCTGTTAC AGAGTTTCAG ATCGGTCCT GATAGTATGT	1380
	ATTTCTTTAG TAAGAATGTG TTAAATTTAC AATGATCTTT TAAAAAGATG ATGCAGTTCT	1440
55	GTATTTATTG TGCTGTGTCT GGTCTAAGT GGAGCCAATT AAACAAGTTT CATATGTATT	1500
	TTCCAGTGT TGAATCTCAC AACTGTACT TTGAAAAATTT CCTTCCATCC TGAATAACGA	1560
60	ATAGAAGAGG CCATATATAT TGCCTCCTTA TCCTTGAGAT TTCCTACCT TTATGTTAAA	1620

AGTTGTGTAT AATTGTTAAA ATCTGTGAAA GAATAAAAAG TGGATTTAAZ TTAAAAAAA 1680
AAAAA AAA 1693

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(2) INFORMATION FOR SEQ ID NO: 222:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1196 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

ACGCGTGGGT CGACCCACGC GTCCGCGACN TGGCGTGGTG GGAAGGGAG AAGGATTTGT 60
AAACCCCGGA GCGAGGTTCT GCTTACCCGA GGCGCTGCT GTGCGGAGAC CCCC GGTTGA 120
AGCCACCGTC ATCATGTCTG ACCAGGAGGC AAAACCTTCA ACTGAGGACT TGGGGGATAA 180
GAAGGAAGGT GAATATATTA AACTCAAAGT CATTGGACAG GATAGCAGTG AGATTCACCT 240
CAAAGTGAAA ATGACAACAC ATCTCAAGAA ACTCAAAGAA TCATACTGTC AAAGACAGGG 300
TGTTCCAATG AATTCACCTA GGTTCCTCTT TGAGGGTCAG AGAATTGCTG ATAATCATA 360
TCCAAAAGAA CTGGGAATGG AGGAAGAAGA TGTGATTGAA GTTTATCAGG AACAAACGGG 420
GGGTCAATCA ACAGTTTAGA TATCTTTTTT ATTTTTTTTC TTTCCCTCA ATCCTTTTTT 480
ATTTTTAAAA ATAGTTCTTT TGTAAATGTTG TGTTCAAAAC GGAATTGAAA ACTGGCACCC 540
CATCTCTTTG AAACATCTGG TAATTTGAAT TCTAGTGCTC ATTATTCATT ATGTTTGT 600
TTCATTGTGC TGATTTTTGG TGATCAAGCC TCAGTCCCTC TCATATTACC CTCTCCTTTT 660
TAAAAATTAC GTGTGCACAG AGAGGTCACC TTTTTCAGGA CATTGCATTT TCAGGCTTGT 720
GGTGATAAAT AAGATCGACC AATGCAAGTG TTCATAATGA CTTTCCAATT GGCCCTGATG 780
TTCTAGCATG TGATTACTTC ACTCCTGGAC TGTGACTTTC AGTGGGAGAT GGAAGTTTTT 840
CAGAGAACTG AACTGTGGAA AAATGACCTT TCCTTAACCT GAAGCTACTT TTAATTTTG 900
AGGGTCTGGA CCAAAGAAG AGGAATATCA GGTGGAAGTC AAGATGACAG ATAAGGTGAG 960
AGTAATGACT AACTCCAAAG ATGGCTTCAC TGAAGAAAAG GCATTTTAAG ATTTTTTAAA 1020
AATCTTGTC GAAGATCCCA GAAAAGTTCT AATTTTCATT AGCAATTAAT AAAGCTATAC 1080
ATGCAGAAAT GAATACAACA GAACACTGCT CTTTTTGATT TTATTTGTAC TTTTGGCCT 1140
GGGATATGGG TTTTAAATGG ACATTGTCTG TACCAGCTTC ATTAAAATAA ACAATA 1196

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(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TCAGGGAGGT GGCAGGAAAG GCTTGGAACA GCTGCCGGAG TGACGGAGCG GCGGCCCCGC 60
CCGGTTGCGC TGGAGGTCTG AGCTTCCAGG TAGCGGCCCG CAGAGCCTGA CCCAGGCTCT 120
15 GGACATCCTG AGCCCAAGTC CCCACACTC AGTGCACTGA TGAGTGCGGA AGTGAAGGTG 180
ACAGGGCAGA ACCAGGAGCA ATTTCTGCTC CTAGCCAAGT CGGCCAAGGG GGCAGCGCTG 240
20 GCCACACTCA TCCATCAGGT GCTGGAGGCC CCTGGTGTCT ACGTGTTTGG AGAACTGCTG 300
GACATGCCCC ATGTTAGAGA GCTGGCTGAG AGTGACTTTG CCTCTACCTT CCGGCTGCTC 360
ACAGTGTTTG CTTATGGGAC ATACGCTGAC TACTTAGCTG AAGCCCGGAA TCTTCCTCCA 420
25 CTAACAGAGG CTCAGAAGAA TAAGCTTCGA CACCTCTCAG TTGTCAACCT GGCTGCTAAA 480
GTAAAGTGTA TCCCATATGC AGTGTGCTG GAGGTCTTGC CCTGCGTAAT GTGCGGCAGC 540
30 TGAAGACCT TGTGATTGAG GCTGTGTATG CTGACGTGCT TCGTGGCTCC CTGGACCAGC 600
GCAACCAGCG GCTCGAGGTT GACTACAGCA TCGGGCGGGA CATCCAGCGC CAGGACCTCA 660
GTGCCATTGC CCGAACCTG CAGGAATGGT GTGTGGGCTG TRAGGTGCTG CTGTCAGGCA 720
35 TTGAGGAGCA GGTGAGCCGT GCCAACCAAC ACAAGGAGCA GCAGCTGGGC CTGAAGCAGC 780
AGATTGAGAG TGAGGTTGCC AACCTTAAAA AAACCATTAAGT TACGACG GCAGCAGCAG 840
40 CCGCAGCCAC ATCTCAGGAC CCTGAGCAAC ACCTGACTGA GCTGAGGGAA CCAGCTCCTG 900
GCACCAACCA GCGCCASCCA GCAAGAAAGC CTCAAAGGGC AAGGGGCTCC GAGGGAGCGC 960
CAAGATTTGG TCCAAGTCGA ATTGAAAGRA CTGTGTTTTC CTCCTTGGG ATGTGGGGTC 1020
45 CCAGCTGCCT GCCTGCCTCT TAGGAGTCCT CAGAGAGCCT TCTGTGCCCC TGGCCAGCTG 1080
ATAATCCTAG GTTCATGACC CTTACCTCC CTAACCCCA AACATAGATC ACACCTTCTC 1140
50 TAGGGAGGAG KCAAATGTAG GTCATGTTTT TGTGGTACT TTCTGTTTTT TGTGACTTCA 1200
TGTGTTCCAT TGCTCCCCGC TGCCATGCTC TCTCCCTGT TTCTTAAGA GCTCAGCATC 1260
TGTCCTGTT CATTACATGT CATTGAGTAG GTGGGTAGCC CTGATGGGG TCCTCTGTC 1320
55 TGGAGCATAA CCCACAGCG TTTTCTCTGC CACCCCATCC CTGCATGCCT GATCCCCAGT 1380
TCCTATACCC TACCCCTGAC CTATTGASCA GCCTCTGAAG AGCCATAGGG CCCCCACCTT 1440
60 TACTCACACC CTGAGAATTC TGGAGCCAG TCTGCCATGC CAGGAGTCAC TGGACATGTT 1500

CATCCTAGAA TCCTGTCACA CTACAGTCAT TTCTTTTCCT CTCTCTGGCC CTGGGTCTCT 1560
 GGAATGCTG CTGCTTCAAC CCCAGAGCCT AAGAATGGCA GCCGTTTCTT AACATGTTGA 1620
 5 GAGATGATTC TTCTTTGGCC CTGGCCATCT CGGGAAGCTT GATGGCAATC CTGGAAGGGT 1680
 TTAATCTCCT TTGTGAGTT TGGTGGGGAA GGAAGGGTA TATAGATTGT ATTAAAAAAA 1740
 10 AAAAGGTATA TATGCATATA TCTATATATA ATATGACGCA GAAATAAATC T 1791

15 (2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2517 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

25 AACTAGTGG ATCCAAAGAA TTCGGCACAG CGGCACAGCA TTGTTGAGCT TTCTGTGTG 60
 TGTGGGGCCC TCAAGCGAGC TCGACTGGTC CATCTGGGG TAGCGASGTG GTGTTTGTGA 120
 AAAAGGACGA TGCCATCACC GCATAYAAGA AGTACAACAA CCGGTGTCTG GACGGGCAGC 180
 30 CGATGAAGTG CAACCTTCAC ATGAATGGGA ATGTTATCAC CTCAGACCAG CCCATCCTGC 240
 TCGGCTGAG TGACAGCCCA TCAATGAAAA AGGAGAGCGA GCTGCCTCGC AGGGTGAAC 300
 35 CTGCTCCTC CTCCAACCCC CCTGCCGAAG TGGACCTGA CACCATCCTG AAGGCACCTC 360
 TCAAGTCCTC AGGGGCTCTC KTGACCACGC AGCCACAGA WITCAAAATC AAGCTTTGAG 420
 CAGGGGAGTR AGGCAGCCAG AAGTGGGGC AGAGGAGGGT GGCTCTGTTT CCCCAGGCA 480
 40 AAGCTTATGA CCAATGGGCC ATCGACTGG AGACCCCTGA TTGTGGGAAG GGTGCCAGG 540
 GATAAAGAGC TTCTCACTG GATGGGACCC GCCTTTCTGT GTGTGTCTT GCCCTGTGCT 600
 45 CTTCCTCTA CGTTAACGTT TCCTGTAGTA TGTTCCTTCA TCTCATCGCC AAGGTAGGCT 660
 TGTGTTTMM AGTGTGTGCC TCCCCGAGCC TCAGCCCCAA GCTGATTCTT TATCTGGAAA 720
 TGGTACACTG AATTCCTCTG GTGGCTTTCT TGTGGCCCCA TGGGATGCAG CGTGGGGCT 780
 50 GTCTGAAGGA CCCTGCTTTT TCCAGGGGCC GAGGGGCTGC CTTCCTTTG TGTGTATTAA 840
 GCTTTTCAAA CAATGAGGG GATGGAGAGC CCTGGGTGCC TGACGGGAGC CAGGTCGGCC 900
 55 TGAGAGCTGT GCCGCTCCTC TGTCTTGTC GTGGAGGTGC CTGGGTGGGG AGCAGGTCTC 960
 AGGCCTCTTG TCCTCTCCCC AGTGGCTCCA GCCTCACTA GTGGCAAGGG CAGGATGAGG 1020
 CTGCACCGCT GGAAGAGTC TATCTAAGCT CTGGCTTGG AGTCCCGTGT CGTCTCCGCC 1080
 60

CAGAGGAAGT TCTCCAGAGT TCACCTTTCC CTMTTCCTTG AGTTGTGCTG AATGCCCCAC 1140
 CCCAGCTCTC TTTCCCTTCT GGGTGTCTTT GCTGGGAGGG GGCTGTGTTG TGAGCCCTCC 1200
 5 CGGTTCCTCAC CTCGCTGGC ACTTAACCAC ACCCTGGTTT TGTGTAGCCG CCAGCTCTCT 1260
 TCTGGTTGGG CCTTTGAAAG GCTCAGCCTC CCATTGTGCA GTGCTTGGGT TTGGAGCTTA 1320
 10 TTTGAATGGA AGAGGTCAGT TTGTTCCTGG CTCTCCATTT CTGGCCTCAG TTGTCTACAG 1380
 GACAGTGGTC AGGGATGCCT GGAGGCATAT ATCCAGCTGC CACCAAGGGG CACTGTTTGT 1440
 TCCCCTTAT GTGAGTGACC CCATCCATCC ATGACCAGAG GATTATTTTC CTGCCTTGGC 1500
 15 AGAGGAGGAG GAGTCAAGGG AGCAGGGCAG CTCTACCAGG CAAGGTGTTT CCCCAGCATA 1560
 GGCGCAGACA GTTGGGACGA AACTTCAGAG CCCAGGCAGT CCCTGAATGA CCAGGCCAGT 1620
 GTTGTCACTG AGTGGTCCCC TGCTGGTTGG GAGTGAAGAG AATCCAGGCT GGCAGAGCTG 1680
 20 GAGCCAGTTG GGGAGCACGG TTCTGGGAGC TCTGCAAAAT CAGTAGCAAG TGCTGGAAAA 1740
 GGCACATGCC GAAGATACTC AAGAGCTCCC AAGATTTGCT TGAGGCTAGC CCAGTAAAA 1800
 25 AAACCAGAGA CTCATGTTTC CAGGGGTCAG TCTGTCAGGC AGGAAGGACC CAGGATTTGA 1860
 ACCCAGCTTC AGTGTGCAGG CTCTGAGGCT GCCCAGGACG GGAAAGTCCA AGGAAGGGGC 1920
 CTGGTGGTGC TCCACTTGCA GTTCTTTAAA GAATGCTGCT TTTATTTCTC CTAACCTTT 1980
 30 CAAGTGGGTG CAGACTTCTC GTTAGCAGCT GGAAGACATT CCTCCACAC TTTTCCCTTC 2040
 CTGGCCCAAG AGAGCATCCA GAAGGCAGTA GGACCTGGTT TTTCAGGTAC TGGGAGCCGG 2100
 35 GGGCTCACTG CTTGCACTGT GCTTAGGGTA GGGATGGTAA ATATCCTCCC TGCATGGCTT 2160
 TATCCTCCCT CTCATCCCAA AGCAGGTATC TTCTGGTTGT CACAGAGTTT CATTGAGTCC 2220
 AGCTGCAGCC ACGTGGCCAT CTGGAGCTGG TGCTATAGGT GACCATCTGG TACATTGAGG 2280
 40 GGACCTGTTT GCCTCCTCCA CTCTATAAGC AGTCATCTTG GGAGACCGGG AGGAGAAGGT 2340
 GGTGGGCTAG TCCTGTGTCC TCCTCCACTT CCCATGCCTC TATGTTACCC ATCTGTGTCT 2400
 45 CCTGTGCAGA AGGAGAGGAA GGGCATTAA GAGATGAAGG GTGATTATGT ATTACTTATC 2460
 CATTTCTGAA TAAACATTG TTATTCCTAA AAAAAAAAAA AAAAAACTCG AGGGGGG 2517

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(2) INFORMATION FOR SEQ ID NO: 225:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

	TTGTANCTAA TCGAGGATTG ATTCTAATGA CAGAGTCTTT CAACACTTTG CACATGATGT	60
5	ATCACGAAGC TACAGCTTGC CATGTGACTG GAGATTTAGT AGAACTTCTG TCAATATTTT	120
	TTTCGGTTTT GAAGTCTACA CGCCCTTATC TTCAGAGAAA AGATGTGAAA CAAGCATTAA	180
	TCCAGTGGCA GGAGCGAATT GAATTTGCCC ATAAACTGTT AACTCTTCTT AATTCTTATA	240
10	GTCCTCCAGA ACTTAGAAAT GCCTGTATAG ATGTCCTCAA GGAACCTGTA CTMTTGAGTC	300
	CCCATGATTT TYMTCATACT CTGGTTCCCT TTCTACAACA CAACCATTTGT ACTTACCATC	360
15	ACAGTAATAT ACCAATGTCT CTTGGACCTT ATTTCCCTTG TCRAGAAAAT ATCAAGCTAA	420
	TAGGAGGGAA AAGCAATATT CGGCCTCCGC GCCCTGAACT CAATATGTGC CTCTTGCCCA	480
	CAATGGTGG AACCAGTAAG GGCAAAGATG ACGTTTATGA TCGTATGCTG CTAGACTACT	540
20	TCMTTCTTA TCATCAGTTC ATCCATCTAT TATGCCGAGT TGCAATCAAC TGTGAAAAAT	600
	TTACTGAAAC ATTAGTTAAG CTGAGTGTC TAGTTGCCTA TGAAGGTTTG CCACITCATC	660
25	TTGCACTGTT CCCCAAACCT TGGACTGAGC TATGCCAGAC TCAGTCTGCT ATGTCAAAAA	720
	ACTGCATCAA GCTTTTGTGT GAAGATCCTG TTTTCGCAGA ATATATTAAA TGTATCTTAA	780
	TGGATGAAAG AACTTTTTTA AACACAACA TTGTCTACAC GTTCATGACA CATTTCTTTC	840
30	TAAAGGTTCA AAGTCAAGTG TTTTCTGAAG CAACTGTGC CAATTTGATC AGCACTCTTA	900
	TTACAAACTT GATAAGCCAG TATCAGAACC TACAGTCTGA TTTCTCCAAC CGAGTTGAAA	960
35	TTTCCAAAGC AAGTGCTTCT TTAAATGGGG ACCTGAGGGC ACTCGCTTTG CTCTGTGTCAG	1020
	TACACACTCC CAAACAGTTA AATCCAGCTC TAATTCCAAC TCTGCAAGAG CTTTTAAGCA	1080
	AATGCAGGAC TTGTCTGCAA CAGAGAACT CACTCCAAGA GCAAGAAGCC AAAGAAAGAA	1140
40	AAACTAAAGA TGATGAAGGA GCAACTCCCA TTAAAAGGCG GCGTGTAGC AGTGATGAGG	1200
	AGCACACTGT AGACAGCTGC ATCAGTGACA TGAAAACAGA AACCAGGGAG GTCCTGACCC	1260
45	CAACGAGCAC TTCTGACAAT GAGACCAGAG ACTCCTCAAT TATTGATCCA GGAACGAGC	1320
	AAGATCTTCC TTCCCTGAA AATAGTTCTG TTAAAGAATA CCGAATGGAA GTTCCATCTT	1380
	CGTTTTCAGA AGACATGTCA AATATCAGGT CACAGCATGC AGAAGAACAG TCCAACAATG	1440
50	GTAGATATGA CGATTGTAAA GAATTTAAAG ACCTCCACTG TTCCAAGGAT TCTACCCTAG	1500
	CCGAGGAAGA ATCTGAGTTC CCTTCTACTT CTATCTCTGC AGTTCTGTCT GACTTAGCTG	1560
55	ACTTGAGAAG CTGTGATGGC CAAGCTTTGC CCTCCCAGGA CCCTGAGGTT GCTTTATCTC	1620
	TCAGTTGTGG CCATTCAG AAGACTCTTTA GTCATATGCA GCAACATGAC ATTTTAGATA	1680
	CCCTGTGTAG GACCATTGAA TCTACAATCC ATGTCGTCAC AAGGGATATC TGGCAAAGGA	1740
60	AACCAAGCTG CTTCTTGACA TTAGGTGTAG CATGTCTACT TTAAAGTCCC TCACCCCAA	1800

CCCCCATGCT GTTGTATATA GTTGTGCTTA TTTGTTTTTG TGCTTCAGTT TGTCCAGTGC 1860
 TCTCTGCTTG AATGGCAAGA TAGATTTATA GGCTTAATTC TTGGTCAGGC AGAACTCCAG 1920
 5 ATGAAAAAAA CTTGCATCTT CAGTATACTT CCTAAAGGGC AATCAGATAA TGGATATGTT 1980
 TTATGTAATT AAGAGTTCAC TTTAGTGGCT TTCATTTAAT ATGGCTGTCT GGAAGAACA 2040
 10 GGGTTGCCTA GCCCTGTACA ATGTAATTTA AACTTACAGC ATTTTACTG TGTATGATAT 2100
 GGTGTCTCT GTGCCAGTT TGTACCTTAT AGAGGCAGAT TGCCTCCGAT CGCTGTGGTT 2160
 CTTATTATCA AAATTAAGTT TACTTGTATA CGGAACAACC ACAAGAAATT TGATTCTGTA 2220
 15 AAGAATCCTC TTTAGCTGTG GCCTGGCAGT ATATAAATGG TGCTTTATTT AACAGAATAC 2280
 CTGTGGAGGA AATAAGCAC ACTTGATGTA AAAATAATTG TTTTATTTT ATTGACATGA 2340
 20 CTGATTGATT GCTATTCTGT GCACTNAATT AACTTGATTG TGATGACTTA AAAAAAAAAA 2400
 AAAAAAAAAA AAAAAAAAAA AAAA 2424

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(2) INFORMATION FOR SEQ ID NO: 226:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ATATAGGACG GATAATCTGT TTACATTCTG TTCTTCTCGA TGCACTCACA AGCGGGTAAC 60
 TAGGTGACAA GAAAACAAAG ATCTTATTCA AAAGAGGTCT TACAGCAACC CAACGTCTCA 120
 40 TCTTCCATA GTAAAGATGA CGGCGCTTG AGGTAAGCTA CAGGCAACAC CACTTCCGCG 180
 TTTCTCTTGC GCCCTGGTCC AAGATGGCGG ATGAAGCCAC GCGACGTGTT GTGTCTGAGA 240
 45 TCCCGGTGCT GAAGACTAAC GCCGACCCC GAGATCGTGA GTTGTGGGTG CAGCGACTGA 300
 AGGAGGAATA TCAGTCCCTT ATCCGGTATG TGGAGAACA CAAGAATGCT GACAACGATT 360
 GGTTCGACT GGAGTCCAAC AAGGAAGGAA CTCGGTGGTT TGGAAAATGC TGGTATATCC 420
 50 ATGACCTCCT GAAATATGAG TTTGACATCG AGTTTGACAT TCCTATCACA TATCCTACTA 480
 CTGCCCCAGA AATTGCAGTT CCTGAGCTGG ATGGAAAGAC AGCAAAGATG TACAGGGGTG 540
 55 GCAAAATATG CCGTACGGAT CATTTCAAAC CTTTGTGGGC CAGGAATGTG CCCAAATTTG 600
 GACTAGCTCA TCTCATGGCT CTGGGGCTGG GTCCATGGCT GGCAGTGGAA ATCCCTGATC 660
 TGATTCAGAA GGGCGTCATC CAACACAAAG AGAAATGCAA CCAATGAAGA ATCAAGCCAC 720
 60

TGAGGCAGGG CAGAGGGACC TTGATAGGC TACGATACTA TTTTCCTGTG CATCACACTT 780
 AACTCATCTA ACTGCTTCCC CGGACACCCCT CCACCTCTAG TTGTTACTAA GTAGCTGCAG 840
 5 TAGGCATTGC TGGGGAAGAA ACAAACACAC ACCAAACAGT ACTGCTACTT AGTTTCTAAG 900
 GCTGCACAGG GAAGGGAAAG ACTGGGCTTT GGACAATCTA GAGGTAATTT ATATCCGCCC 960
 CCAGGTGGAG CAACATGCGA TTCTGGAGGC ACGGGGGTAA CTGAAAGTGA GTACATATAG 1020
 10 TCTTCTGGT TTCTGGAGAT AACCCATCAA TAAAAGCTGC TTCCTCTGGG TAAAAAAAAG 1080

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(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

25

TTGCATTCAC AATTACTGGG AGGCAGGCAG GGCAGTTGC ATGCTGGGGG TGGCTGCATG 60
 GSCTGCCASC TCTCTGGGT TTGAAGGATG CGGTACASCT GCTTCAGCTG AGCAACGATG 120
 30 TTATCCTTGA TGTCTGGGGT TGAGATCTGC AGGCGGACAC TGCCACTATC AAAGGATCGT 180
 GTGAAATCAC CAGAAAACAT CTCGTAGATC ATCCGAGCCA CTACTGGAAT GACCTGAACC 240
 AAGATGAGTT TCCTTTCCAA TGGTTTCCCA TCTGGCCATT CTTCCCCAAA GCATAAGTAG 300
 35 ATCTCAAACG GTGGCTGCTT CTCTATCTGT CTTTCTGGT GGGCAATGAG ATCGCTAAGG 360
 AATGTTTCCA GACAAAATAG CTTGACCTTC TTTTGTCTCT CAATCAGGTT GGGAGCAACA 420
 40 AGTGATGGGG CACATGGCCC AGACCACTAC ACCTTGCACT GGCACAGYCT GATGGCATAA 480
 ATGGCATGAC CGCTGACCTC CAGGATCAGT CCTCTGTCCA TGACGTCCAG CAGCTTGCTA 540
 GTGAACAGCT TCTGCTTCTC ATTGGTAATA TGCTCAGGAC CTGGGAATTT GACCTGCTCC 600
 45 AGNCTGACGG GACCAAAGAG CTCCTCCTGG TCAGGCATGG GACCCAGGTC CCCATAGAAG 660
 AGTCGGCAGC CCTGAGGGTT GCTCAGGTC ATGGTCCTGC CCGTACTCCT TCCCACGGTA 720
 50 CTGAAACTTG ATGTCCAGGT CAGTCATTGG GAGAGAGCTG ATCCACAGTT CTGGAGAGCT 780
 ATAGAAGGRC TGTATAGGTG CCTGGGGWAC TTCCATCTCC AGGGGTCAG TTTTGGGCCA 840
 CACTGCCTCC GGSCTGCAGT TGCCACACT GCAATTGCCC ACACTGGCTG GCGCCATGGG 900
 55 AGAACCATTG ATGTTCAAGG AGGGGAAGGT GTCTGGATG GGAACATGGT GCTGCGACTG 960
 ATCCAGCTCA TCTTCTCAT CTTCTTCATC CACATCATTA TCCTTCTCAT CCCAGGGAGC 1020
 60 AGACCCTGTG GATCCTGGGT TAATGATCGA SCCCTGGGGC TGAGGGATGT CACACACTTG 1080

ATATATCTTC ACTGGGTTCA TGGGCACCTC CCTGGTGCC ATCCATACAT CCAGGTGAA 1140
TTCTCTGCTC TTATTGAGAG CACAGCGCAG CTGGGCCTTC CATTTAGCTG GGTCAGGGTC 1200
5 ATCCACCCCT TCCTGGTACT TCCCTGTCTC TACAGCCCAG GCCTTAAAAA TGGTATTTTC 1260
CTCTTCTTGT TGAGGGCTAT GCCGGGTGGC ATGTTTCCAG GGAATCTGGA AGCGTTTAGA 1320
10 GTCCCTGTGT AGCCAG 1336

15 (2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2043 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

25 TCAGCTGGTC CCTTCCTTGT GTCCCTGGGG ACCTGCTGGC GGCTCTTCC TGGGAGCCAT 60
GACCTCAGAC CCCACCCACA CTCCAGATCG AGACCCCTGC CTCCCCCCGG CAAATGTCCT 120
CCCCGTGCCT TGCAGCCTGC ACTTTGCACA TGCTCACCCC CAGCACAGTC CCACTGGCCC 180
30 CTCAMCTCCC CTTCCTGAG CTCCCTCCCA AGGACTCCTG GTCACTGCCT GCTGTGCAKT 240
CAGAGGCCCA GGTCCAGCA GCCCGSGGG AACGGGTGCT GCCTSTTCCT CCAGTTAGCT 300
35 CCAGYTCAGG TCTGAGACCC GTGYTGAGTA AAGGTCTGAG CAMCGACCGT GCCCTCTGCC 360
CAGGGCTGGG TCCTGAGCAG CTGGTTTCC TGCAGGAAGG TTGGAGCAAG CAAAGTCCTT 420
CTCTGCCCTC AGGGTCAGCT GCCCAGACTG GGGCGGATGC AGAGAGGCAG GTGGGCTGTG 480
40 GCTGGACTGG TCCGGAGCTG GCTTCCTTAC CAGAAAAGCC TCAGCCTTCC TCTGGAAGCA 540
TCCCCCGTTC TGGGCAAGGG GGAAGGGCTC CTTTAAGGGG TGTGCTTTC CAGTGGGGAG 600
45 CAGTCTGGCC CTGCCCCCTA CTAAAGCCTC TGCTCTCAGC ACTTCCCCC AAGTCCTTGT 660
AACTTGCTTG AAGGTGGGT CTGGCTGCCA GCCAGTCCCT GGACAACTC TCCTGCCCCCT 720
TTTAAATTTT ACTCATTTTG TATAAACCCA GCAGGCTGGT GTTTACTTAG CCCTGTAGCT 780
50 TTTTTCATTT TTTCTTCCG TCTTCTTCT TGAGTTCACG GTTCAATATT GCCTCCTCGC 840
CCTGGTGAGG GGAGGTGCTG CTTTCTGCC CCACCTGCCG GCTGGTCCA GCAGCGCTGG 900
55 NGCCAGCTG GGGGGCCGG ATGGGGGCTT CTCTCTCTGG GAGGGGTGCA GGTGCCCTCC 960
CCAGGCTGGG AGGGTTCCTT CCCTAGCTCC CCATCTGCCC CCGCTGGTGA GAGTTGGGCT 1020
TCTTGGTCTT GGAACCTCCT GGCATTGGGA ACAGAGCATT TCCAGCATTT GTTGTGTGTG 1080
60

	TTTACTCAC CTAACCTTA GAAAATGAAT GTTAGAAGGT GCCTGCCGAG GCGGGACAGA	1140
	GTGTTTGCTC GCGCTGGAGA AGGCTCTGCT CAGCCCTGAG AGTCCCTTCC TGCCCCACCG	1200
5	ATACTGGCAC TTTAAAAAGG AAGCTGACCG CACAGTGTCC AGACGAATTG GCGCCAGAA	1260
	GATGGGGAGT TCTGTCTGC CTTCTGTGT CTGCGTGACC TCACCCAGCC TAGGAGGGAG	1320
	GTGCATTGAG GGTAGATTG CTTCTCATTC AAAGTTCTGG GGCTTTGGGY GGAAAACAGC	1380
10	CAGCTTTGGC GCTGTTGGG AGACTCCTCC AGACCAGGAA CCCCAGAAGG AGACAGAGCC	1440
	TGCCACATCC TCCCACGCCA GGCCCTGGGC CAGGGTGATT GGAAGTGAAG TTTGGCCACA	1500
15	ACCAAATTGA TGCTGGCTGG AACCAGAGGC CAGAAAGCCT GGCTTTGTCC CCATGTGGGA	1560
	GCCCTGTCTT CAGCCCTCTT GTCCCTTGA GCTCAGTGA TTCCCACCAG GTGCCCACAG	1620
	CTCCTGGACT TCAAATTTCTA TATATTGAGA GAGTTGGAGA GTATATCAGA GATATTTTGT	1680
20	GAAAGGAGTT GGTCTATGCA ATGTCAGTTT GGAATCTTCT TGAAAGTTTA ATGTTTTTAT	1740
	TAGGAGATT AAAGAAAATA AAGGTCTACA ATATCTTTAG GTTTTTTTTT TTTCTGTCT	1800
25	ACCGCACAAA CTGACCACAT GGCATGTCTA TCAGGATGGA GGGTGTCCAT GTTCTCTCT	1860
	GTCTTTAGGG AGGTGATAAG GAGATGGSCG RAGGGGTGTT TTTTCTTTG ACTCCCTCC	1920
	TTTCTAACAG AATGTTGCCA CCACTGCTTG AGTGGGCTGT GTTGTTCCT CTGTCCCAGC	1980
30	TTCTGTTGTA GAAAATAACA TTGTTAGGG AACTCAGGCT AGTGTACAGC TCTTGGTTG	2040
	GGG	2043
35		

(2) INFORMATION FOR SEQ ID NO: 229:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

	TAAAAAGAAG CGGAGAATC TGGCGTCGC TCTAGAGATC GATGGGCTAG AGGAGAAGCT	60
50	GTCCCAGTGT CGGAGAGACC TGGAGGCCGT GAACTCCAGA CTCCACAGCC GGGAGCTGAG	120
	CCCAGAGGCC AGGAGGTCCC TGGAGAAGGA GAAAACAGC CTAATGAACA AAGCCTCCAA	180
	CTACGAGAAG GAACTGAAGT TTCTTCGGCA AGAGAACCGG AAGAACATGC TGCTCTCTGT	240
55	GGCCATCTTT ATCCTCCTGA CGCTCGTCTA TGCCTACTGG ACCATGTGAG CCTGGCACTT	300
	CCCCACAACC AGCACAGGCT TCCACTTGGC CCCTTGGTCA GGATCAAGCA GGCACCTCAA	360
60	GCCTCAATAG GACCAAGGTG CTGGGGTGT CCCCTCCCAA CCTAGTGTTC AAGCATGGCT	420

TCCTGGCGGC CCAGGCCTTG CCTCCCTGGC CTGCTGGGGG GTTCCGGGTC TCCAGAAGGA 480
CATGGTGCTG GTCCCTCCCT TAGCCCAAGG GAGAGGCAWT AAAGACACAA AGCTGGAAAT 540
5

10 (2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

AATGTGAAA TATTAGAATA TTGTTACTAT TTGACCCAAC TCAAAATCTC CATGGGAAAA 60
20 TACCTGTGCA TACCCACAGT ATTGTTGAAA ATAATCAGAT GCAGTATCAC AGCTGTGTCA 120
GACTCTAGTA CCAGTTGGGC AATCAAGGCA CAGCTAAAAA TTGAAAACAA AGATCTGGAC 180
25 AACAAAACAG CCAAAGGTGG GGGTCAAGAA GCTCTGACGT GTACCTAGCT GTAGAATGCT 240
ATGCACACGT GCCAGGTGTA GTGTGCATAT CCAGGAAAAA CTGCAGAGAG CCCCAGTCTT 300
CAMCTCTGGT TGACCATGAG CTCTGTGTAA GCAGGAAGTG AAGGCTAAGG CAGATTTAAG 360
30 CTCTGAAAGC ATTCCACAAC ATACACACAA ATCGTGCAAA GCATTAAGGA AATCTTGTTA 420
CTGCTAAGTG TTGCTGACCC AGGAACAA 448
35

(2) INFORMATION FOR SEQ ID NO: 231:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GTATGCTGCC CCAAACCAAT ATGTGTGGCT GCCTTTWACC TGACTTCTCC AACATGTAGC 60
50 CCCAAGAGGA GGCCTCTAGA CTRAGGGAGG GGCTGGTGAC CCAGGTGTGG TGGGGCTGCA 120
TGARACTACC AGAGAGACAG ACATTCTGGA ACTCACCTG GGGGATCCAG TGGATCTGCC 180
TATGGTCTGG TCCACCCAG ACCTGTGAGA TGTTCCTCAT GAGGATGCAC TTGTGCTTCT 240
55 GCAAGTATTG CTGCAGCTTC ATAGTGACTC CCACCAGCAC CAGCAATACA GYTAGCTACC 300
TGTGGCCTTG GATCTCAGCC AGCATGGCTG GGAGAGGGAG CARCTGGGCA TGTACCCTAA 360
60 ATGCTGTTAC CAGGGAAGGA CTCCAGAGT GAAGACAAGT AGGGACT 407

5 (2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

15 GTATTTGATT TCAGGCTGCT AAATGGGCTC ATTTAGCATT CATTCCTTGA TG TAGACATT 60
AAAAAAAAA CTGAATAGCA TTCTTTCCAG GNTAACTAAT AAAGCAGACA TGCTAAGCCT 120
ATAAATACAT CAGCACTGCA GCACACGTTT AAGGTTGCCA CGGACAAGGA TCACACAATA 180
20 GAGAACTG TAGTTCGGTC TGCTCACAAG ACCCAGAACA TTGATCAGTT TTTGTGTGTG 240
GTTTATTATT TTCTGTAA AAAATTGTGA AAAGTTTGT TTAGCTAGAT GATATTTTAA 300
25 TAGCTGCGAG TGCTTTGGAA CTATAAAGAT GTCACTACTT AACACACATA CCTTATGTTT 360
TGTTTGTGTT TGTTTACAC TCAGTATAAA TCAGGAGAAG TTAGCCAACC ATCTAGCATT 420
TAGAATCCTC TTTTATATG TCTTCTAAGG ATATGGATGT TCCCATAACA GCAACAAAAC 480
30 AGCAACAAAA ACATTTTATA AATATCACTT GATAGACTGT AAGCACCTGC TTAACCTTGT 540
GTNCCAAATA TTAGTGTGT ATATATATAT ATATATACAC ACACACACAC ATATATATTC 600
35 AACAAATAAA GCAAATATA ACATGCATTT CACATTTTGT CTTTCCCTGT TACGATTTTA 660
ATAGCAGAAC TGTATGACAA GTTTAGGTGA TCCTAGCATA TGTTAAATTC AAATTAATGT 720
AAAACAGATT AACAACAACA AAGAACTGT CTATTGAGT GAAGTCATGC TTTCTATTAT 780
40 AATAACTTGG CTTCCGTTAT CCATCAAATG CACACTTATA CTGTTATCTG 830

45

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

55 CCAGAAGAAA GACCAATCTA GAATATGGAA CTCTAATCAC TTCTAGTATT TCAACTTCCT 60
AGCAGAAATG AACTTGGCCC TAGACCTAGG GGATAAGCAA TGTTCTTTAT GTAGCCAATG 120
60 CTACGGAAAC AAAAGAGGTG AAAGAGACCC TTTTTTATA CTTAATGTAC ATATATTGAC 180

TTTTGTGAGCA AGAATGCCAG AAATAGCCTT CATTTCTACC CTGCAAAATA ATCCAGATCT 240
 GCTTTCTAAA ATGRANTCAG TTTCTAAAGT GAAACATGCA ATATTTATGC TCTGACTGAC 300
 5 TCCTGAATTG GARGAGGAAG RACTTCTGTT TACAGAAAAC YGTATTGTTA TATATGTCAG 360
 GCTGTGTATT GTGACTATCA GCATTCTGGT GCAAATGAAC TTTTCTCCAT CATCGACTGT 420
 10 GGAAAATGA TACTTTTAAA GCATATCTTT CTATGAGCAC AGGTCCTCCT AGTGAAACTT 480
 AATTTGACAA AGGGTGTGAT ATGCTTTCCT AACCTGAWTT GTATTAACAT TCACAGAGCC 540
 TACATTTTCT CATTAGGGTT RTGATGCTCA GTATCTTTCC AAGTGCCAGG CAGRGCTTNC 600
 15 CTTTCTGAT CAAACATACC ATTTTGTGA TTTCACAACT ATAGACAGTC ACTTCTGCAG 660
 TCCCAATTGA AAAATGCAGA ACTGCTTTAT CCAAGAATGC TGAAAAATAC TGTCTATCC 720
 20 AGGTTTCTTA AACTATAAAA GCAGATTTTG CTTTGTGTTG TTAATCATAG GCATGGCCGA 780
 GCATTGTGGA TTAGCCTGAG GCTTAAATC AGATGCATGT CTGGTAAGAT GACCACTGTC 840
 TCACTATCAA GAGCCTGCAG AGCCATTTTC CAGACCTGTG ATTGCCCAGA ACACATAGTC 900
 25 CCCACGTTTC TAATTTGGAG CAAATCTAAA AG 932

30

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2786 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

40 TTAGCAGGGT GAGCTGTTAA AACAGCACAC ATCTCTCATC CCTCTTCCT TTATTCCTCC 60
 CTGGGTTTCA GAAAGGAAGG ATATATGGG ACCACCTCCC CCTTCTTTGA TCCCAGCATC 120
 45 TCAGTCCCCC TCCCAACCCT CCATATGGCT CTCAATGGTG CTCACTTGCT TGGAAGCAGG 180
 CTCCAATAG GGAGGGGCT GCCCTCTACA GTCTCTTTGA CTGTAAGACA GGGCTCTGTA 240
 TCAGTGAGAC GATGAGAAAA GTCCCAGGCT AATGGCAGAA ATTTGCACTT TGAACATGTG 300
 50 TGTFTTTGTG TTGTGGAACC TGAGATTCTT TATTTATTA CAGGAAGTCT GATTTTMTT 360
 TTTTGGAGTC TTTGTGCTA TATTTGTGG GGCTGGGAGA GAGAGATTAG ATTATTTTGA 420
 55 CATGGGATCC CTTCCATAAC AGGTACTTTG AAGGCAAGAC ATAGGGTTGA AGAAGCACAA 480
 CCAGCTCTG AAATCATAGC TCTCCAGTGG CTTTAAAGA AAGCTGGTCC TCAGCACTAA 540
 CAAAATCACT ACAATAGCCT AGTGCTTTTT TGGAAGCCTT TTTAGGAAG AATGTTAGGT 600
 60

	TCATGGTAAC TAGTATGCTC TTTGAGATTT TTACAGTGT T GAAACTTAAG AATTTTGAGA	660
	GGGTGAGGAG GGTGTTCAG AATCTAAAT ACAGATAGAT GATTGTTTCT TGTGAATTTG	720
5	TTTCTTTTCC TTTTTTTTTG TCCCTACCAT TTCCTTACAT TTCCCTTGGG GCCCATCTCT	780
	GGCTCCTTGC TTTTGTTC TTGCTTTGCT TTATCAGTTC ATTCCAGCTC CCTGTTAGTG	840
10	AAGGACACTG CTGTTAGTGA AGGAACAAAG TCTATGAGTC CTAAAATTTT AAGTCAAAGA	900
	AAACTGCTCT GTTCCCTT TAGTAACACT TCTGAAGAGG AAAAATTCA ATAGCCAAAG	960
	TTAATAATCC TATATAATAA TTGCTTTGGC TTTCACCTAA AATTCTGGGC ATCACAATTT	1020
15	CCTTGGGATA GAGGTGTGT TGGGAATAG ATTGCTTATT GCTGTTCACT GGAGAGAAAA	1080
	GGTAGTGT TGTACAAG TCATACCGCC AGAAGCCCCA AATCCTATTT TGGCTCATCT	1140
20	TCAGGTAAAG AGTAATTCCT ATCCTGTGTG CCTCAGAAGC TAGAATCGAA GGCTTACCTT	1200
	ATTCATTGTT TATTGTCAGA AATGCATGAT GGCTCTTGA AAGAATGACG TTTTGTGGA	1260
	AAAAAAAAA AGAACAGTTT GTGTTTCACA AACATGGCTT ATCAATTTT TCAAAGAATT	1320
25	CTTTTTTCCC AAAAAGAGGA GTAACAAAT GTCATTTCTG AAAGAGGCTT ACTTTATACC	1380
	AACTAGTGC AGCATTGGG ATGCCAGGA ACAGAGAGTG AGACACCTAC AATCACCAGT	1440
30	CTCAAATGCG CTATTGTTT TTTTCAGAGT GTTGCAGATT TGCCATTTCT CCATAATATG	1500
	GGGATAGAAA ATGGAATAA GATAGAAGG ATGTAGAATA TGCTTTCCTG CCAACATGGT	1560
	TTGGAGTGA CTTTGGTATA TTGACTAGAT TTGAAAATAC AAGATTGATT AGATGAATCT	1620
35	ACAAAAAGT TGTCTCCTC TCAGGTCCCT TTTACACTTT TTGACTAACT AGCATCTATA	1680
	TTCCACACTT AGCTTTTTTG TCACACTTAT CCTTGTCTC CGTAAATTTT ATTTGCAGTG	1740
40	GTTAGTCATC AGATATTTTA GCCACCTACA CAAAGCAAA CTGCATTTT AAAATCTTT	1800
	CTGAGATGGG AGAAAATGTA TTCTCCTTTC CTATACCGCT CTCCAACAA AAAACAAC	1860
	AGTTAGTTCT ACTAATTAGA AACTTGCTGT ACTTTTTCTT TTCTTTTAGG GGTCAAGGAC	1920
45	CCTCTTTATA GCTACCATTT GCCTACAATA AATTATTGCA GCAGTTTGCA ATACTAAAAT	1980
	ATTTTTTATA GACTTTATAT TTTTCTTTT GATAAAGGA TGCTGCATAG TAGAGTTGGT	2040
50	GTAATTAAAC TATCTCAGCC GTTCCCTGC TTTCCCTTCT GCTCCATATG CCTCATGTC	2100
	CTTCCAGGA GCTCTTTTAA TCTTAAAGTT CTACATTTCA TGCTCTTAGT CAAATTCGT	2160
	TACCTTTTA ATAACCTTC CCACTGCATA TTCCATCTT GAATTGGTGG TTCTAAATTC	2220
55	TGAAACTGTA GTTGAGATAC AGCTATTTAA TATTTCTGGG AGATGTGCAT CCTCTTCTT	2280
	KGTGGTTGCC CAAGTTGTT TTGCGTAACT GAGACTCCTT GATATGCTTC AGAGAATTTA	2340
60	GGCAAACACT GGCCATGGCC GTGGGAGTAC TGGGAGTAAA ATAAAAATAT CGAGGTATAG	2400

ACTAGCATCC ACATAGAGCA CTTGAACCTC CTTTGTACCT GTTTGGGGAA AAAGTATAAT 2460
GAGTGTACTA CCAATCTAAC TAAGATTATT ATAGTCTGGT TGTTTGAAAT ACCATTTTTT 2520
5 TCTCCTTTTG TGTTTTCCC ACTTTCCAAT GTACTCAAGA AAATGAACA AATGTAATGG 2580
ATCAATTITAA AATATTTTAT TTTTAAAAG CCTTTTTCG CTGTGTAAAT GTGCAGGACC 2640
CTTCTCCTTT CATGGGAGAG ACAGGTAGTT ACCTGAATAT AGGTTGAAAA GGTATGTAA 2700
10 AAAGAAATTA TAATAAAGG GATACCTTGC TTTTCAAATC TTTGTTTCT CTTATTCTAG 2760
GTAAGGCATA TTAATAATAA ATATGT 2786

15

(2) INFORMATION FOR SEQ ID NO: 235:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 458 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

GGGTGCAGGA ATTCGGCAG AGAGAATGTT TGATTTCCTT TCCTATTTTA AGGATCTTCT 60
30 CTCTTGTTGA TGTGAAAAC TTACCTTAGT GAAGATGTGT TTCAACATGC TGTGTCTCTT 120
TACCTGCATA ATCACAGCTA TGCATCTATT CAAAGTGATG ATCTGTGGGA TAGTTTAAAT 180
GAGGTCACAA ACCAAACACT AGATGTAAAG AGAATGATGA AAACCTGGAC CCTGCAGAAA 240
35 GGATTTCTTT TAGTGACTGT TCAAAGAAA GGAAAGGAAC TTTTATACA ACAAGAGAGA 300
TTCTTTTAA ATATGAAGCC TGAAATTCAG CCTTCAGATA CAAGGTACAT GCCCTCTTTC 360
40 TTTTCATGCC ATCTCTTTTG CACTCTCAGG TGGAAATATT TTAAAGTGT TTATAATCAT 420
AAGTTCTTGT GAAACCTAAC AAGATTATCC CTTCCTAA 458

45

(2) INFORMATION FOR SEQ ID NO: 236:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

AGGATGAAGA GGAAATTATC TCTTGATTG CTCTCCAGGA AATCCTTCTC TATACTTTAA 60
AAGCTCTTGT TCTTTTCTAG GARTCCAATG TGCTGATTGC TGCTAACAGT CAGGGTACAA 120
60

	TTAAGGTGCT AGAATTGGTA TGAAGGGTTA ACTCAAGTCA AATTGTACTT GATCCTGCTG	180
	AAATACATCT GCAGCTGACA ATGAGAGARG AAACAGAAAA TGTCATGTGA TGTCTCTCCC	240
5	CAAAGTCATC ATGGGTTTGT GATTTGTTTT GAATATTTTT TCTTTTTC TTKTCCCTCC	300
	TTTATGAGCC TTTGGGACAT TGGGAATACC CAGCCAACTC TCCACCATCA ATGTAACCTC	360
10	ATGGACATTG CTGCTCTTGG TGGTGTATC TAATTTTGT GATAGGGAAA CAAATTCCTT	420
	TGAATAAAAA TAAATAACWA AACAATAAAA GTTTATGAG CCACAGTTGA GCTTGGAAG	480
	TTTTTGTCAA ATGCGCAAG AGATAACTCT TTTTANGAAG TAGCATATGT GAACTATAAT	540
15	GTAACAGTGA ATAATTGTGA AAGTTCGTAT TTCCCAACCT CTTTGGGAAT T	591
20	(2) INFORMATION FOR SEQ ID NO: 237:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1286 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:	
30	TCTTTTAAAG GTACAGCAGG GAAGAACTGG AAACCTCAGAG AAAGAACTG CCCTTCCATC	60
	TACAAAAGCT GAGTTTACTT CTCTCCTTC TTTGTTCAAG ACTGGGCTTC CACCGAGCAG	120
35	GAGATTACCT GGGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG	180
	CAGGCGACGG GCAAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA	240
	AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTTCCTT CCAGGAGCTC CTCCCACTCA	300
40	CCTTCCACCT CCTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT	360
	TCCACCACCG GGTTCCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT	420
45	AGAAAGTGGA CATTCCTCTG GTTATGATAG TSGTCTGCA CGTGCAATTTC CATATGGCAA	480
	TGCGATGAAG AACGATACAG ATACAGGGAA TATGCAGAAA GAGGTTATGA GCGTCACAGA	540
	GCAAGTCGAG AAAANGAAGA ACGACATAGA GAAAGACGAC ACAGGAGAGAA AGAGGAAACC	600
50	AGACATAAGT CTTCTCGAAG TAATAGTAGA CGTCGCCATG AAAGTGAAGA AGGAGATAGT	660
	CACAGGAGAC ACAAACACAA AAAATCTAAA AGAAGCAAAG AAGGAAAAGA AGCGGGCACT	720
55	GAGCCTGCCC CTGAACAGGA GAGCACCAGG GCTACACCTG CAGAATAGGC ATGGTTTGG	780
	CCTTTGTGT ATATTAGTAC CAGAAGTAGA TACTATAAAT CTTGTTATTT TTCTGGATAA	840
	TGTTTAAGAA ATTTACCTTA AATCTTGTTT TGTGTTTAG TATGAAAAGT TAACTTTTTT	900
60	TCCAAAATAA AAGAGTGAAT TTTTCATGTT AAGTTAAAAA TCTTTGTCTT GTACTATTTT	960

5 AAAAAATAAAA AGACAGCAAT GACTTTATAT CCAAGAAAGG AATGTGAATG AGTCACTTAA 1020
 CAGGGAATCT AAAGAGCTGT GTTAGCTGTG TACATACACA GATTATCTGA GAAAAGGTCA 1080
 AGGGTTCCAC TTGGGCCACA GTTTTTTCT TAATCAAACA CCACTCTCTT AAGRGGCTGC 1140
 ATCACAAARG GCAACCAARG GGCCCTCTT ARGGCTTTGA GGATTAAAC TAGTCTTTAT 1200
 10 CCATTACTGC TGTGGACACT CTGGCTTRG TATWTTTAGG GGGGNTCCTT ACCTTTTTTT 1260
 GGTMTTCNC ACCTTTTTGG TTGGGC 1286

15

(2) INFORMATION FOR SEQ ID NO: 238:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 734 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ATGGCAGCGC AGAAGGACCA GCAGAAAGAT GCCGAGCGG AAGGGCTGAG CGGCACGACC 60
 CTGCTGCCGA AGCTGATTCC CTCCGGTGCA GGCCGGGAGT GGCTGGAGCG GCGCCGCGCG 120
 30 ACCATCCGGC COTGGAGCAC CTTCGTGGAC CAGCAGCGCT TCTCAGGCC CCGCAACCTG 180
 GGAGAGCTGT GCCAGCGCCT CGTACGCAAC GTGGAGTACT ACCAGAGCAA CTATGTGTTC 240
 35 GTGTTCTTGG GCCTCATCCT GTACTGTGTG GTGACGTCCC CTATGTTGCT GGTGGCTCTG 300
 GCTGTCTTTT TCGGCGCCTG TTAACATTCT CTATCTGCGC ACCTTGAGT CCAAGCTTGT 360
 CCTCTTTGGC CGAAAGGTGA GCCCAGCGCA TCATATGCTC TGGCTGGAGG CATCTCCTTC 420
 40 CCCTCTTCTT GGCTGGCTGG TCGGGGCTCG GCCGTCTTCT GGGTGCTGGG AGCCACCCTG 480
 GTGGTCATCG GCTCCACGC TGCCTTCCAC CAGATTGAGG CTGTGGACGG GGAGGAGCTG 540
 45 CAGATGGAAC CCGTGTGAGG TGTCTTCTGG GACCTGCCGG CCTCCCGGGC CAGCTGCCCC 600
 ACCCCTGCCC ATGCCTGTCC TGCACGGTCT GCTGCTCGGG CCCACAGCGC CGTCCCATCA 660
 50 CAAGCCCGGG GAGGGATCCC GCCTTTGAAA ATAAAGCTGT TATGGGTGTC ATTCAAAAAA 720
 AAAAAAAAAA AAAA 734

55

(2) INFORMATION FOR SEQ ID NO: 239:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 809 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

5
CGGGGTCTTC AGGTACCGG GCTGGTTACA GCAGCTCTAC CCCTCAGGAC GCARACATGG 60
CAGCGCAGAA GGACCAGCAG AAAGATGCCG AGGCGGAAGG GCTGAGCGGC ACGACCCTGC 120
10 TGCCGAAGCT GATTCCCTCC GGTGCAGGCC GGGAGTGGCT GGAGCGGCGC CGCGCGACCA 180
TCCGGCCCTG GAGCACCTTC GTGACCAGC AGCGCTTCTC ACGGCCCGC AACCTGGGAG 240
AGCTGTGCCA GCGCCTCGTA CGCAACGTGG AGTACTACCA GAGCAACTAT GTGTTCGTGT 300
15 TCCTGGGCCT CATCCTGTAC TGTGTGGTGA CGTCCCCTAT GTTGTGGTG GCTCTGGCTG 360
TCTTTTTCGG CGCCTGTTAC ATTCTCTATC TGCGCACCTT GGAGTCCAAG CTTGTGCTCT 420
20 TTGGCCGAGA GGTGAGCCCA GCGCATCAGT ATGCTCTGGC TGGAGGCATC TCCTTCCCTT 480
TCTTCTGGCT GGCTGGTGGC GGCTCGGCCG TCTTCTGGGT GCTGGGAGCC ACCCTGGTGG 540
TCATCGGCTC CCACGCTGCC TTCCACCAGA TTGAGGCTGT GGACGGGGAG GAGCTGCAGA 600
25 TGGAACCCGT GTGAGGTGTC TTCTGGGACC TGCCGGCCTC CCGGGCCAGC TGCCCCACCC 660
CTGCCCATGC CTGTCCTGCA CGGCTCTGCT GCTCGGGCCC ACAGCGCCGT CCCATCACAA 720
30 GCCCGGGGAG GGATCCCGCC TTGAAAATA AAGCTGTTAT GGGTGTCAAT CAGGAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA 809

35

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 2201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

TGACCCACG CGTCCGGCAA CATGGCGGCT GCCGTGGTGC AGCGCCCGG CTGAGCGACA 60
GCAAGTGCAG CGGGCTCCTA CCCC GGGTGA GGGGTGGCCT CCGCGTGGCA TCGTGCCCTC 120
50 TTCAGCCCGC TCCTGTCCCC GACATCACGT GTATTCCGCA CGTCCCCTCC GCGCTGTGTG 180
TCTACTGAGA CGGGGAGGCG TGACAGGGCC CGGGTCCCTT CTCAGTGGTG CTCTGTGCTT 240
55 CAGGGCAAGC TCCCCGTCTC CGGGCGCACT TCCCTCGCCT GTGTTCGGTC CATCCTCCTT 300
TCTCCAGCCT CCTCCCCTCG CAGGCGGATG AMCCGGACGA CGGGCCAGTG CCTGGCACCC 360
CGGGGTGGCC ARGGTCCAMG GGAACCCGA AGTCCGAGGA GCCCGARGTC CCGAACCCAG 420
60

	ARGGCTGCA GCGCATCAMC GGCTGTCTC CCGGCCGTTT GGCTCTCATA GTGGCGGTGC	480
	TGTGCTACAT CAATCTCCTG AACTACATGG ACCGCTTCAC CGTGGCTGGC GTCCTTCCCG	540
5	ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG ACCGTGTTC	600
	TCTCCAGTTA CATGGTGTG GCACCTGTGT TTGGCTACCT GGGTGACAGG TACAATCGGA	660
10	AGTATCTCAT GTGCGGGGGC ATTGCCTTCT GGTCCCTGGT GACACTGGGG TCATCCTTCA	720
	TCCCCGAGA GCATTTCTGG CTGCTCCTCC TGACCCGGGG CCTGGTGGGG GTCGGGGAGG	780
	CCAGTTATTC CACCATCGCG CCCACTCTCA TTGCCGACCT CTTTGTGGCC GACCAGCGGA	840
15	CCGGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGGC AGTGGTCTGG GCTACATTGC	900
	AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGGG TGACACCGGG	960
20	TCTAGGAGTG GTGGCCGTTT TGCTGTGTTT CTTGGTAGTG CCGGAGCCGC CAAGGGGAGC	1020
	CGTGGAGCGC CACTCAGATT TGCCACCCCT GAACCCACC TCGTGGTGGG CAGATCTGAG	1080
	GGCTCTGGCA AGAAATCCTA GTTTCGTCTT GTCTTCCCTG GGCTTCACTG CTGTGGCCTT	1140
25	TGTCACGGGC TCCTGGCTC TGTGGGTCC GGCATTCTTG CTGCGTTCCC GCGTGGTCTT	1200
	TGGGAGAGCC CCACCTGCC TTCCCGAGA CTCTGTCTT TCCTCTGACA GTCTCATCTT	1260
30	TGGAATCATC ACCTGCCTGA CCGAGTCTT GGGTGTGGGC CTGGGTGTGG AGATCAGCCG	1320
	CCGGCTCCGC CACTCCAACC CCGGGGTGA TCCCTGGTC TGTGCCACTG GCCTCCTGGG	1380
	CTCTGCACCC TTCTCTTCC TGTCCCTTGC CTGGCCCGT GGTAGCATCG TGGCCACTTA	1440
35	TATTTTATC TTCAATTGGAG AGACCTCTCT GTCCATGAAC TGGGCCATCG TGGCCGACAT	1500
	TCTGCTGTAC GTGGTGATCC CTACCCGACG CTCCACGCC GAGGCCTTCC AGATCGTGCT	1560
40	GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCATT GGCTGATCT CTGACCGCCT	1620
	GCGCCGAAC TGGCCCCCTT CTTCTTGTG CGAGTTCCGG GCTCTGCAGT TCTCGCTCAT	1680
	GCTCTGCGG TTTGTTGGGG CACTGGGCGG CGCACTTTC TGGGCACCGC CATCTTCATT	1740
45	GAGGCCGACC GCGGGCGGC ACAGCTGCAC GTGCAGGGC TGCTGCACGA AGCAGGGTCC	1800
	ACAGACGACC GGATTGTGGT GCCCCAGCG GCGCGTCCA CCGCGTGCC CGTGGCCAGT	1860
50	GTGCTCATCT GAGARGCTG CGCTCACCTA CCTGCACATC TGCCACAGCT GGCCTGGGC	1920
	CCACCCACG AAGGGCCTGG GCTAACCCC TTGGCTGGC CCAGCTTCCA GAGGGACCCT	1980
	GGGCGTGTG CCAGCTCCA GACACTACMT GGGTAGCTCA GGGGAGGAG TGGGGGTCCA	2040
55	GGAGGGGGAT CCTCTCCAC AGGGGCAGCC CCAAGGGCTC GGTGCTATTT GTAACGGAAT	2100
	AAAATTTGTA GCCAGACCCC AGGTGCCTGC TCTCGTCTTT CTCTGGGTGG CCTCTGATCT	2160
60	TGACCCCCGT CTTACCCCA GGGCTCCTGA AGACTGTGGG T	2201

(2) INFORMATION FOR SEQ ID NO: 241:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1661 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

15 GTCTTCCCG ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG 60
 ACCGTGTTCA TCTCCAGTGA CATGGTGTG GCACCTGTGT TTGGCTACCT GGGTGACAGG 120
 TACAATCGGA AGTATCTCAT GTGCGGGGGC ATTCCTTCT GGTCCCTGGT GACACTGGGG 180
 20 TCATCTTCA TCCCCGAGA GCATTTCTGG CTGCTCCTCC TGACCCGGGG CCTGGTGGGG 240
 GTGCGGGAGG CCAGTTATTC CACCATCGCG CCCACTCTCA TTGCCGACCT CTTTGTGGCC 300
 GACCAGCGGA SCGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGGC AGTGGTCTGG 360
 25 GCTACATTGC AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGGG 420
 TGACACCGGG TCTAGGAGTG GTGGCCGTTT TGCTGCTGTT CCTGGTAGTG CGGGAGCCGC 480
 30 CAAGGGGAGC CGTGGAGCGC CACTCAGATT TGCCACCCCT GAACCCACC TCGTGGTGGG 540
 CAGATYTGAG GGCTCTGGCA AGAAATCCTA GTTTCGTCT GTCTTCCCTG GGCTTCACTG 600
 CTGTGGCCTT TGTACGGGC TCCCTGGCTC TGTGGGCTCC GGCATTCTG CTGCGTTCCC 660
 35 GCGTGGTCTT TGGGAGACC CCACCTGCC TTCCCGAGA CTCCTGCTCT TCCTCTGACA 720
 GTCTCATCTT TGGACTCATC ACCTGCCTGA CCGAGTCTT GGGTGTGGGC CTGGGTGTGG 780
 40 AGATCAGCGC CCGYTCCGC CACTCCAACC CCCGGGCTGA TCCCTGGTC TGTGCCACTG 840
 GCCTCCTGGG CTCTGCACC TTCTCTTCC TGTCCCTTGC CTGGCCCGT GGTAGCATCG 900
 TGGCCACTTA TATTTTCATC TTCAITGGAG AGACCTCTCT GTCCATGAAC TGGGCCATCG 960
 45 TGGCCGACAT TCTGCTGTAC GTGGTGATCC CTACCGACG CTCCACCGCC GAGGCCTTCC 1020
 AGATCGTGCT GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCATT GGCCTGATCT 1080
 50 CTGACCGCCT GCGCCGAAC TGGCCCCCT CCTTCTTGTG CGAGTTCCGG GCTCTGCAGT 1140
 TCTCGCTCAT GCTCTGCGG TTTGTGGGG CACTGGGCGG CGCACTTTCC TGGGCACCGN 1200
 CATCTTCATT GAGGCCGACC GCCGGCGGGC ACAGCTGCAC GTGCAGGGCC TGCTGCACGA 1260
 55 AGCAGGGTCC ACAGACGACC GGATTGTGGT GCCCCAGCGG GGCCGCTCCA CCCGCGTGCC 1320
 CGTGGCCAGT GTGCTCATCT GAGAGGCTGC CGCTCACCTA CCTGCACATC TGCCACAGCT 1380
 60 KGCCCTGGGC CCACCCACG AAGGGCCTGG GCCTAACCC TTGGCCTGGC CCAGCTTCCA 1440

5 GAGGGACCCT GGGCCGTGTG CCAGCTCCCA GACACTACMT GGGTAGCTCA GGGGAGGAGG 1500
 TGGGGGTCCA GGAGGGGGAT CCCTCTCCAC AGGGGNCACC CCAAGGGCTC GGTGCTATTT 1560
 GTAACGAAT AAAATTGTGA GCCAGACCCC AGGTGCCTGC TCTCGTCTTT CTCTGGGTGG 1620
 CCTCTGATCT TGCACCCCGT CTTACCCCCA GGGCTCCTGA A 1661

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(2) INFORMATION FOR SEQ ID NO: 242:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

NGACAGAAAA GCAGAAGATG AGACTCTGTT CATTCACTTT TCCTAGGCCC ATCCTGTGGT 60
 25 CATCTTTCCC CCTCCCATCA TACCTCCTCC TTCTGGAGC CTCTGCCGCG TTGGCTGTAA 120
 TGGTGGCACT TACCTGGATA TTTCAGTGGG AGGATGAAAG GCGAGACTCA CCCTACGCGG 180
 TGGGACAGAT GGGGAGAGGA AAAAGGCAGA GATNGCCAGG AGAGGGGTGC AGGACAAACC 240
 30 AGAGAGGTTG GGTGAGGGGA AAAGTGTNGG GAGAAAGTGG GGTGCAGGCC CTGCAGGCCG 300
 GTTTAGCCAG CAGCTGCGGC CTCCCCGGGC CCTTGGCATC CAACTTCGCA GACAGGGTAC 360
 35 CAGCCTCCTG GTGTGTATCA TAGGATTTGT TCACATAGTG TTATGCATGA TCTTCGTAAG 420
 GTTAAGAAGC CGTGGTGGTG CACCATGACA TCCAACCCGT ATATATAAAG ATAAATATAT 480
 ATATATATGT ATGTAAATTA TAGCACTGAG GGCCCTGCTG CCCTGCTGGA CCAAGCAAAA 540
 40 CTAAGCCTTT TGGTTTGGGT ATTATGTTTC GPTTTGTAT TTGTTTGTIT TTGTGGCTTG 600
 TCTTATGTCG TGATAGCACA AGTGCCAGTC GGATTGCTCT GTATTACAGA ATAGTGTITT 660
 45 TAATTCATCA ATGTTCTAGT TAATGTCTAC CTCAGCACCT CCTCTTAGCC TAATTTTAGG 720
 AGGTGCCCCA ATTTTGTTC TTCAATTTTA CTGGTTACTT TTTGTACAA ATCAATCTCT 780
 TTCTCTCTTT CTCTCCTCCC CACCTCTCAC CCTTGCCCTC TCCATCTCCC TCTCCCGCCC 840
 50 TCCCCCTCTC CCTCTGGCTC CCCGTCTCAT TTCTGTCCAC TCCATTCTCT CTCCCTCTCT 900
 CCTGCCTCTT GCTGCCCCCT CCCCAGCCCA CTTSCCGAG TTGTGCTTGC CGCTCCTTAT 960
 55 CTGTTCTAGT TCCGAAGCAG TTTCACTCGA AGTTGTGCAG TCCTGGTTGC AGCTTTCCGC 1020
 ATCTGCCTTC GTTTCGTGTA GATTGACGCG TTTCTTTGTA ATTTCACTGT TTCTGACAAG 1080
 ATTTAAAAAA AAAAAAAGGA AAAAAA AAAA AAAAAC TCGAGGGGGG GCCCGGTACC 1140
 60

CAATTG

1146

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(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

15	AACCCACGGC TGCTGCGCA GGGCGTGGAG GGCAGAGGCG CGCGGAGGCG CAGTTGCAAA	60
	CATGGCTCAG AGCAGAGACG GCGGAAACCC GTTCGCCGAG CCCAGCGAGC TTGACAACCC	120
20	CTTTCAGCCA CCACCAGCCT ATGAGCCTCC AGCCCCTGCC CCATTGCCTC CACCCTCAGC	180
	TCCCTCCTTG CAGCCCTCGA GAAAGCTCAG CCCACAGAA CCTAAGAACT ATGGCTCATA	240
	CAGCACTCAG GCCTCAGCTG CAGCAGCCAC AGCTGAGCTG CTGAAGAAAC AGGAGGAGCT	300
25	CAACCGAAG GCAGAGGAGT TGGACCGAAG GAGNCGAGAG CTGCAGCATG CTGCCCTGGG	360
	RGGCACAGCT ACTCGACAGA ACAATTGGCC CCCTCTACCT TCTTTTGTG CAGTTCAGCC	420
30	CTGCTTTTTC CAGGACATCT CCATGGAGAT CCCCCAAGAA TTTCAGAAGA CTGTATCCAC	480
	CATGTACTAC CTCTGGATGT GCAGCAGGCT GGCTCTTCTC CTGAACCTCC TGCCTGCCT	540
	GGCCAGCTTC TGTGTGGAAA CCAACAATGG CGCAGGCTTT GGGCTTTCTA TCCTCTGGGT	600
35	CCTCCTTTTC ACTCCCTGCT CCTTTGTCTG CTGGTACCGC CCCATGTATA AGGCTTTCCG	660
	GAGTGACAGT TCATTCAATT TCTTCGTTTT CTCTTTCATT TTCTTCGTCC AGGATGTGCT	720
40	CTTTGTCTC CAGGCCATTG GTATCCAGG TTGGGGATTG AGTGGCTGGA TCTCTGCTCT	780
	GGTGTGCGG AAGGCAACAC AGCAGTATCC GTGCTCATGC TGCTGGTCGC CCTGCTCTTC	840
	ACTGGCATTG CTGTGCTAGG AATTGTCTAT CTGAAACGGA TCCACTCCTT ATACCGCCGC	900
45	ACAGGTGCCA GCTTTCAGAA GGCCAGCAA GAATTTGCTG CTGGTGTCTT CTCCAACCTT	960
	GCGGTGCGAA CCGCARCTTG CCAATGCAGC CGCTGGGGCT GCTGAAAATG CCTTCCGGGC	1020
50	CCCGTGACCC CTGACTGGGA TGCCCTGGCC CTGCTACTTG AGGGAGCTGA CTTAGCTCCC	1080
	GTCCCTAAGG TCTCTGGGAC TTGGAGAGAC ATCACTAACT GATGGCTCCT CCGTAGTGCT	1140
	CCCAATCCTA TGGCCATGAC TGCTGAACCT GACAGGCGTG TGGGGAGTTC ACTGTGACCT	1200
55	AGTCCCCCCA TCAGGCCACA CTGCTGCCAC CTCTCACAG CCCCACCCA GCTTCCCTCT	1260
	GCTGTGCCAC GGCTGTGCT TCGGTTATTT AAATAAAAAG AAAGTGAAC TGGAAAAAAA	1320
60	AAAAAAAAA AAAAAAAG GGGGNCCTNC	1350

5 (2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

15 TCCCAGAGGC CGGGGGGTTC CAGCTCTGCC TGTAGCAGAG CCCTGAGGAG GAGGAGGAAG 60
AGGATGTGCT GAAATACGTC CGGGAGATCT TTTTCAGCTA GGGCATAAAC TGTGCACTGA 120
ACTGTCCTGCC GAGAGCAGCT GGAGGACAGC TGAGCTTCCA CTGGTGCTGC TGGGCCGACC 180
20 GCCTGTGGGA ATGGGGCTCT CTGTGCTCCT ACCTTTGTGC CTTCTTGGGC CTGGCAGATT 240
CACCTCAGGC CAGAAGCCCC TGGACACTCC GGGCCTTGGG GTGCCGTTCT GAGTGTGCGG 300
25 AAGGCAGGAC TCAAATGAG ATCCCATTTG ACTCCCTCTG TATGTAAGT GCCCTCTCCT 360
GGCTCTGAG GCTCTGGAGT CCCAATTGTC TGTGTTAGTC AGTGACCAGG TTCCAGGGAA 420
AATRATGTCA TGTGGTGGTC CAACTTACTG GAACCAAAGA GACAGTACTT TGCAAAGAAA 480
30 AGGATCACTG CCAGGTGCAC TGGAATTGCT ACAGTTTAGT CCGCATGATC TCTCCTGAAG 540
GAGGAAGCCT GTTTCAAAAA TAGTTTCCAT CATGAGTCTA TCAATGAGCT CCCACCTCTC 600
35 CAGCCAGCCT AGAAAGCAAA CGAGCTGCCC ACAGTTCTCT GCCCTGTCTG GGAGGTTGAG 660
GCCACAGTGT ATAGACTGGT AAGCCAGACA GGCTCTCTCC CGCAAGCTGC TACCTTGCTT 720
TCACCTGTAC CTTGGTCCCC GGGCAGCTAG CTATAAGCA AGAGGGACAG GAGCCAGAA 780
40 GAGACACTGA GGACAAGAGA TCACACCAGA GTACATGTCT CTGCCTCTGT TTTCAGTGTG 840
GCTTTGGACA GGAATATATG AATAAATCAC TGCCATACAG GTTTTCCAAT ACACAAGTGC 900
45 TAGAAAATAC ACACAATTCC CCAATGCGTA AGTTGTGCTA ATGTCTTTCC AAGTTCTGGG 960
TTGGGAAGTG GAGGGTGGCA GCGTTTGTTC GTGCGCAACC GTCCAGTCTT GTTCACAGCG 1020
AGGATTTGGA GTCCTCCAGG GTCTCATCAT GGGAGTGATT TGTACGCGA CGCCTCTGCC 1080
50 CTGTCTGGCT TCAGGTCCAG GGAAGCTTTG AAGCAGTCAA GCCTTGCTTT TGTACCCCAT 1140
GTGTCTGTG TTTGTTGAGT CACTCAGAGA TCACTCTGG ACCTCTGGGG TTGGAGTTCC 1200
55 AGTGATGGCT TATGGCGGCC CACTCACTAT GGTGGGCTGA GTGAAGCTC CTTAACCATG 1260
TCCCCAGAGA CACTGAGGTG CTCGCTCTTT TAATGTCCTC GTTTGTTGCC GTAAGTTCTT 1320
TGCTAGGTTT CATTTTGCCA TTTGGCAAAT CAGCCTGGAA GTCTGGCCCC ATGACAGCAA 1380
60

TCACTCCCTC CCCACCCCTCC TGAAGCTAGA GGAAGATTTG CTCAGATCCA TTAATTAAAG 1440
 CAGGAATTGG TGTGACAATG AGCTGCATGG TTTAGGGAGT CTTTGGGAGC CTTGGAAGTC 1500
 5 CTGAAGGACA AACAACTCTG TACTAAGAA 1529

10 (2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1537 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

20 GTGCGAGGTC CCCGCCAGCC CCCAGCGGCC TTCCCGGCC GGGCGGCTCC CAGAGCAAAC 60
 GAGGCCCTG AGAGCTCCAC CTAGTTCACA GGATAAAATC CCACAGCAGA ACTCGGAGTC 120
 AGCAATGGCT AAGCCCCAGG TGGTTGTAGC TCCTGTATTA ATGTCTAAGC TGTCTGTGAA 180
 25 TGCCCTGAA TTTTACCTT CAGGTTATTC TTCCAGTTAC ACAGAATCCT ATGAGGATGG 240
 TTGTGAGGAT TATCCTACTC TATCAGAATA TGTTCAGGAT TTTTGAATC ATCTTACAGA 300
 30 GCAGCCTGGC AGTTTTGAAA CTGAAATTGA ACAGTTTGCA GAGACCCTGA ATGGTTGTGT 360
 TACAACAGAT GATGCTTTGC AAGAACTTGT GGAACATC TATCAACAGG CCACATCTAT 420
 CCCAAATTTC TCTTATATGG GAGCTCGCCT GTGTAATTAC CTGTCCCATC ATCTGACAAT 480
 35 TAGCCACAG AGTGGCAACT TCCGCCAATT GCTACTTCAA AGATGTCGGA CTGAATATGA 540
 AGTTAAAGAT CAAGCTGCAA AAGGGGATGA AGTTACTCGA AAACGATTTT ATGCATTTGT 600
 40 ACTCTTCTG GGAGAACTTT ATCTTAACCT GGAGATCAAG GGAACAAATG GACAGGTTAC 660
 AAGAGCAGAT ATTCTTCAGG TTGGTCTTCG AGAATTGCTG AATGCCCTGT TTTCTAATCC 720
 TATGGATGAC AATTTAATTT GTGCAGTAAA ATGTGTTAAAG TTGACAGGAT CAGTTTGTGA 780
 45 AGATGCTTGG AAGGAAAAAG GAAAGATGGA TATGGAAGAA ATTATTCAGA GAATTGAAAA 840
 CGTGTCTCTA GATGCAAACT GCAGTAGAGA TGTA AACAG ATGCTCTTGA AGCTTGTAGA 900
 50 ACTCCGGTCA AGTAACTGGG GCAGAGTCCA TGCAACTTCA ACATATAGAG AAGCAACACC 960
 AGAAAATGAT CCTAACTACT TTATGAATGA ACCAACATTT TATACATCTG ATGGTGTTC 1020
 TTTCACTGCA GCTGATCCAG ATTACCAAGA GAAATACCAA GAATTACTTG AAAGAGAGGA 1080
 55 CTTTTCCTCA GATTATGAAG AAAATGGAAC AGATTTATCC GGGGCTGGTG ATCCATACTT 1140
 GGATGATATT GATGATGAGA TGGACCCAGA GATAGAAGAA GCTTATGAAA AGTTTGTGTT 1200
 60 GGAATCAGAG CGTAAGCGAA AACAGTAAAG TTAAATTTCG GCATATCAGT TTTATAAAGC 1260

AGTTTAGGTA TGGTGATTTA GCAGAACACA AGAGAGCAAG AAAATGTGTC ACATCTATAC 1320
 CAAATTRAGG ATGTTGAGTT ATGTTACTAA TGTATGCAAC TTTAATTTTG TTTAACACTA 1380
 5 TCTGCCAAAA TAAACTTTAT TCCCTATAAC TTAAATGTG TATATATATA TAATAGTTTA 1440
 TTATGTACAG TTAATCTAC TGTMTGGCT GCAATAAAAT CGATTTTGAA ATAAAWRAAA 1500
 10 AAAAAAAAAA AAGGNGGCC GCTCTAGAG ANCCAAG 1537

15 (2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

25 TGCAGGATTT GGCCAGGACC CSCCGCGTG GCGGTGCTA TCGCTTCGCA GAACCTACTC 60
 AGGCAGCCAG CTGAGAAGAG TTGAGGGAAA GTGCTGCTGC TGGGTCTGCA GACCGGATGG 120
 ATAACGTGCA GCCGAAAATA AAACATCGCC CCTTCTGCTT CAGTGTGAAA GGCCACGTGA 180
 30 AGATGCTGCG GCTGGATATT ATCAACTCAC TGGTAACAAC AGTATTCATG CTCATCGTAT 240
 CTGTGTTGGC ACTGATACCA GAAACCACAA CATTGACAGT TGGTGGAGGG GTGTTTGCAC 300
 35 TTGTGACAGC AGTATGCTGT CTGCCGACG GGGCCCTTAT TTACCGGAAG CTTCTGTTCA 360
 ATCCAGCGG TCCTTACCAG AAAAGCCTG TGCATGAAA AAAAGAAGTT TTGTAATTTT 420
 ATATTACTTT TTAGTTTGAT ACTAAGTATT AAACATATTT CTGKATTATT CCAAAAAAAAA 480
 40 AAAAAAAAAA AAAAAAATT TGGTGG 506

45

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1348 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55 GTCTTCTTT TNCTGTTTG AGTTGGTGAG TGAGTGAATA GGGTAACATG GGCCTTCAGG 60
 ATGACCCCTT GGAAGTGTGC CGAGTTCCTT AAATCTCAGC TGGGATCCTG GACCTGGGAG 120
 60 GCCCCTGTGA GGGCCAGCTC TGA AAAACC TGGGAGTTGA TGCCGAGGY TGGGAAGAAC 180

TCTGCTCGAG GGCAGGGTGC CCTGGAACAC TGGTAGTTCT GGGGCTGGGA GGGAGAGGGG 240
 CTCCGGCTTT CTCTGAAATG AACACTGCTC TTCAGCAGTT CAAGTACTTG TTCTCAAAAC 300
 5 ATTTTCTAAT TGATTGGTAG GTTTTCATAA GCATTGTTTC TTTAAGGCAT GGAAAGGGAA 360
 GAATGCTCAA GCAAGTCATG TTTGTTTTCA GTGGGATGGG CCCGCGTTCT CACTGCTGGG 420
 10 GGCTTCCCCT TGCATGTGGC ACCTTTGTGC AGGGCCACCA GGCAGACTCT TCCCACCTTC 480
 TCCCCTGAA GCACCAAGGG GCTTGAACCG TAATTGGCT AATCAGAGGC ATTTTMTTGT 540
 TCCTAGTATC TTTCACACTT GTCCAACCGT CTTATMTTMT TAAAAGTTCT GTTGCTGTGA 600
 15 TTAACACGAA ACTAGAGAGA AATAGTTTCT GAAGCCAGTT TATTGTGAAG ATCCCAAGG 660
 GGAGGTTCCG TAGAGAAAAA TAGTAAGCTG GTTTAGAAAC TGACGAGGGC AAACAGCCAG 720
 20 GACGCATTGG AGAGGAATTT GCCAAAGATC TACCCTGAGA TAACGCCTGT CCAGTGTCTT 780
 CACCACGTGA ATAACCAGCG CTCCAAAGTG TTTTCTGCT TTGAAAAAA AAATTCACA 840
 AGCTTTTAAA GGTGCATTTA AGAATCCATG TGACTTTAGA ATGGAAGTGC CGGCCCTGGC 900
 25 AACTGTCACG TGTGCTAGAA GGTTCGATGC CTCTGGAATG CATGTGATAC TCATCTCCAT 960
 TTTGTTTCCT TGATTGCATT TTTGTTCTTT TAGCAGATCT GTCCCTGTGG GTGGTGTCTA 1020
 30 AGAAGTCGGA CACCTTGGTT TTTGTGTTAG ATTGAGCTGG GCAGCTGCAA TCAGCTTCTT 1080
 TATATGCAA TTAGGCACGA CCCATCTGTG GTTCCTGGT TGGTGGCTAA TGAAGTGAGG 1140
 GGAGGGAGGG ATGTCACCCC AAAAGTAGGC CCTCCCATMG GCTTTGGCCA GGCCAGACAC 1200
 35 TTCACATCGT TTACATGGTT CTGTGTAAAT TTAAAGTTTA TGTGTATAAA GCGAAGCTGT 1260
 TTCTGTGAAA CTGTATATTT TGTAATAAAA TATATGCTA CTTTGAGAWR AAAAAAAAAA 1320
 40 AAAAATCGA GGGGGGCCG GTACCCAA 1348

45 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1766 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

55 GTGCCGAATC GGCAGAGCGG CACGAGCGGC CACGAGAGCA GGCGAGTAA AGGGACTTGA 60
 GCGAGCCAGT TGCCGGATTA TTCTATTTCC CCTCCCTCTC TCCCGCCCCG TATCTCTTTT 120
 60 CACCTTCTC CCACCTCGC TCGGTASCA TGGCGAGCG TCGCGGCCA CTCAGTCCCA 180

	TTCCATCTCC TCGTCGTCTT TCGGAGCCGA GCCGTCCGCG CCCGGCGGCG GCGGGAGCCC	240
	AGGAGCCTGC CCCGCCCTGG GGACGAAGAG CTGCAGCTCC TCCTGTGCGG TGCACGATCT	300
5	GATTTTCTGG AGAGATGTGA AGAAGACTGG GTTTGTCTTT GGCACCACGC TGATCATGCT	360
	GCTTTCCCTG GCAGCTTTCA GTGTCATCAG TGTGGTTTCT TACCTCATCC TGGCTCTTCT	420
10	CTCTGTCACC ATCAGCTTCA GGATCTACAA GTCCGTCATC CAAGCTGTAC AGAAGTCAGA	480
	AGAAGGCCAT CCATTCAAAG CCTACCTGGA CGTAGACATT ACTCTGTCTT CAGAAGCTTT	540
	CCATAATTAC ATGAATGCTG CCATGGTGCA CATCAACAGG GCCCTGAAAC TCATTATTCG	600
15	TCTCTTCTG GTAGAAGATC TGGTTGACTC CTGAAGCTG GCTGTCTTCA TGTGGCTGAT	660
	GACCTATGTT GGTGCTGTTT TTAACCGAAT CACCCTTCTA ATTCTTGCTG AACTGCTCAT	720
20	TTTCAGTGTC CGATTGTCT ATGAGAACTA CAAGACCCAG ATTGATCACT ATGTTGGCAT	780
	CGCCCGAGAT CAGACCAAGT CAATTGTTGA AAAGATCCAA GCAAACTCC CTGGAATCGC	840
	CAAAAAAAG GCAGAATAAG TACATGGAAA CCAGAAATGC AACAGTTACT AAAACACCAT	900
25	TTAATAGTTA TAACGTCGTT ACTTGTACTA TGAAGGAAAA TACTCAGTGT CAGCTTGAGC	960
	CTGCATTCCA AGCTTTTMTT TTAATTTGGT GTTTTCTCCC ATCCTTTCCC TTTAACCTC	1020
30	AGTATCAAGC ACAAAAATTG ATGGACTGAT AAAAGAACTA TCTTAGAACT CAGAAGAAGA	1080
	AAGAATCAAA TTCATAGGAT AAGTCAATAC CTTAATGGTG GTAGAGCCTT TACCTGTAGC	1140
	TTGAAAGGGG AAAGATGGA GGTAAAGAG AAAATGAAAG AACACCTCTG GGTCTTCTG	1200
35	TCCAGTTTTC AGCACTAGTC TTACTCAGCT ATCCATTATA GTTTTGCCCT TAAGAAGTCA	1260
	TGATTAACTT ATGAAAAAAT TATTTGGGGA CAGGAGTGTG ATACCTTCCT TGGTMTTMTT	1320
40	TTGCAGCCCT CAAATCCTAT CTTCCTGCCC CACAATGTGA GCAGCTACCC CTGATACTCC	1380
	TTTTCTTTAA TGATTTAACT ATCAACTTGA TAAATAACTT ATAGGTGATA GTGATAATTC	1440
	CTGATTCCAA GAATGCCATC TGATAAAAAA GAATAGAAAT GGAAAGTGGG ACTGAGAGGG	1500
45	AGTCAGCAGG CATGCTGCGG TGGCGGTCAC TCCCTCTGCC ACTATCCCCA GGGAAGGAAA	1560
	RGCTCCGCCA TTTGGGAAAG TGGTTTCTAC GTCAGTGAC ACCGGTTCTG AGCATTAGTT	1620
50	TGAGAACTCG TTCCCGAATG TGCTTTCTCT CCTCTCCCT GCCACCTCA AGTTTAATAA	1680
	ATAAGGTTGT ACTTTTCTTA CTATAAAATA AAAAAAAAAA AACTCGAGGG GGGCCCGGTA	1740
	CCCAAATCGC CGGATATGAT CGTAAA	1766
55		

(2) INFORMATION FOR SEQ ID NO: 249:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2664 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

	AGTGTCTCTCG GAGCAGGCGG AGTAAAGGGA CTMGAGCGAG CCAGTTGCCG GATTATTTCTA	60
10	TTTCCCCCTCC CTCTCTCCCG CCCCGTATCT CTTTTCACCC TTCTCCCACC CTCGCTGGCG	120
	TASCATGGCG GAGCGTCGGC GGGCACTCAG TCCCATTTCCA TCTCCTCGTC GTCCTTGGGA	180
15	GGCGAGCCGT CCGCGCCCGG CGCGGGGGG AGCCCAGGAG CCTGCCCCGC CCTGGGGACG	240
	AAGAGCTGCA GCTCCTCCTG TCGGGTGCAC GATCTGATTT TCTGGAGAGA TGTGAAGAAG	300
	ACTGGGTTTG TCTTTGGCAC CACGCTGATC ATGCTGCTTT CCCTGGCAGC TTTCAGTGTC	360
20	ATCAGTGTGG TTTCTTACCT CATCTGGCT CTTCTCTCTG TCACCATCAG CTTCAGGATC	420
	TACAAGTCCG TCATCCAAGC TGTACAGAAG TCAGAAGAAG GCCATCCATT CAAAGCCTAC	480
25	CTGGACGTAG ACATTACTCT GTCCTCAGAA GCTTTCCATA ATTACATGAA TGCTGCCATG	540
	GTGCACATCA ACAGGGCCCT GAAACTCATT ATTCGTCTCT TTCTGGTAGA AGATCTGGTT	600
	GACTCCTTGA AGCTGGCTGT CTTCATGTGG CTGATGACCT ATGTTGGTGC TGTPTTTTAA	660
30	GGAATCACCC TTCTAATTCT TGCTGAACTG CTCATTTTCA GTGTCCCGAT TGTCTATGAG	720
	AAGTACAAGA CCCAGATTGA TCACTATGTT GGCATCGCCC GAGATCAGAC CAAGTCAATT	780
35	GTGTAAAAGA TCCAAGCAAA ACTCCCTGGA ATCGCCAAAA AAAAGGCAGA ATAAGTACAT	840
	GGAAACCAGA AATGCAACAG TTAATAAAAC ACCATTTAAT AGTTATAACG TCGTTACTTG	900
	TACTATGAAG GAAAATACTC AGTGTGAGCT TGAGCCTGCA TTCCAAGCTT TTTTTTTTAA	960
40	TGGTGTITTT CTCCCATCCT TTCCCTTTAA CCCTCAGTAT CAAGCACAAA AATTGATGGA	1020
	CTGATAAAAG AACTATCTTA GAACTCAGAA GAAGAAAGAA TCAAATTCAT AGGATAAGTC	1080
45	AATACCTTAA TGGTGGTAGA GCCTTTACCT GTAGCTTGAA AGGGGAAAGA TTGGAGGTAA	1140
	GAGAGAAAAT GAAAGAACAC CTCTGGGTCC TTCTGTCCAG TTTTCAGCAC TAGTCTTACT	1200
	CAGCTATCCA TTATAGTTTT GCCCTTAAGA AGTCATGATT AACTTATGAA AAAATTATTT	1260
50	GGGACAGGA GTGTGATACC TTCTTTGGTT TTTTTTTGCA GCCCTCAAAT CCTATCTTCC	1320
	TGCCCCACAA TGTGAGCAGC TACCCCTGAT ACTCCTTTTC TTTAATGATT TAACTATCAA	1380
55	CTTGATAAAT AACTTATAGG TGATAGTGAT AATTCCTGAT TCCAAGAATG CCATCTGATA	1440
	AAAAAGAATA GAAATGAAA GTGGGACTGA GAGGGAGTCA GCAGGCATGC TGCGGTGGCG	1500
	GTCACCTCCCT CTGCCACTAT CCCGAGGAA GGAAARGCTC CGCCATTTGG GAAAGTGGTT	1560
60	TCTACGTCAC TGGACACCGG TTCTGAGCAT TAGTTTGAGA ACTCGTTCCC GAATGTGCTT	1620

	TCCTCCCTCT CCCCTGCCCA CCTCAAGTTT AATAAATAAG GTTGTACTTT TCTTACTATA	1680
5	AAATAAATGT CTGTAACTGC TGTGCACTGC TGTAACTTG TTAGAGAAAA AAATAACCTG	1740
	CATGTGGGCT CCTCAGTTAT TGAGTTTMTG TGATCCTATC TCAGTCTGGG GGGGAACATT	1800
	CTCAAGAGGT GAAATACAGA AAGCCTTTT TTCTTGATCT TTTCCCGAGA TTCAAATCTC	1860
10	CGATTCCCAT TTGGGGGCAA GTTTTTTTTCT TCACCTTCAA TATGAGAATT CAGCGAACTT	1920
	GAAAGAAAAA TCATCTGTGA GTTCCTTCAG GTTCTCACTC ATAGTCATGA TCCTTCAGAG	1980
15	GGAAATATGA CTGGCGAGTT TAAAGTAAGG GCTATGATAT TTGATGGTCC CAAAGTACGG	2040
	CAGCTGCAAA AAGTAGTGGA AGGAAATGT CTACGTGTCT TGGAAAAATT AGTTAGGAAT	2100
	TTGGATGGGT AAAAGGTACC CTGCGCTTAC TCCATCTTAT TTTCTTAGCC CCTTTGAGT	2160
20	GTMTTAACTG GTTTCATGTC CTAGTAGGAA GTGCATTCTC CATCCTCATC CTCTGCCCTC	2220
	CCAGGAAGTC AGTGATGTC TMTTGGGCT TCCCTCCAA AGGACCTTCT GCAGTGAAG	2280
25	TGCCACATCC AGTTCMTTC TTTTGTGCT GCTGTGTTA GATAATTGAA GAGATCTTTG	2340
	TGCCACACAG GATTTTTTTT TTTTTTAAGA AAAACCTATA GATGAAAAAT TACTAATGAA	2400
	ACTGTGTGTA CGTGTCTGTG CGTGCAACAT AAAAATACAG TAGCACCTAA GGAGCTTGAA	2460
30	TCTTGGTTCC TGTAATAATTT CAAATMGATG TGGTATTAAT AAAAAAAAAA AAAACAMAAA	2520
	AAAAAAAAAA AAAAGGGCGG CCGCTCTAGA GGATCCAAGC TTACGTACGC GTGCATGCGA	2580
35	CGTCCATAGC TCTTTCTATA GGGGTCCCCC AAATTCATT CANCGGGCCG TCGGTTTTAN	2640
	AAAGGTCGTG ANTGGGGGAA ANCC	2664

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(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

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CGTGGGAGTG AGGTACCAGA TTCAGCCCAT TTGGCCCCGA CGCCTCTKTT CTCGGAATCC	60
GGGTGCTGCG GATTGAGGTC CCGGTTCTTA ACGGTGGGAT CGGTGTCCTC GGGATGAGAT	120
55 TTGGCGTTTC CTCGGGCTTT TGGTGGGATC GGTGTCCTCA GGATGAGATT TAGGGTTTCC	180
TCGGGGCTTT CGGGATCTTC ACCTAATATC CGGACTGCAA GATGGAGGAA GCGGGGAACC	240
TAGGAGGCCT GATTAAATG GTCCATCTAC TGGTCTTGTC AGGTGCCTGG GGCATGCAAA	300

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TGTGGGTGAC CTTCGTCTCA GGCTTCCTGC TTTTCCGAAG CCTTCCCCGA CATACCTTCG 360
 GACTAGTGCA GAGCAAATC TTCCCCTTCT ACTTCCACAT CTCCATGGGC TGTGCCTTCA 420
 5 TCAACCTCTG CATCTTGGCT TCACAGCATG CTGGGGCTCA GCTCACATTC TGGGAGGCCA 480
 GCCAGCTTTA CTGCTGTTC CTGAGCCTTA CGCTGGCCAC TGTCAACGCC CGCTGGCTGG 540
 10 AACCCCGCAC CACAGCTGCC ATGTGGGCCC TGCAAACCGT GGAGAAGGAG CGAGGCCTGG 600
 GTGGGGAGGT ACCAGGCAGC CACCAGGCTC CCGATCCCTA CCGCCAGCTG CGAGAGAAGG 660
 ACCCCAAGTA CAGTGCTCTC CGCCAGAATT TCTTCCGCTA CCATGGGCTG TCCTCTCTTT 720
 15 GCAATCTGGG CTGCGTCTG AGCAATGGGC TCTGTCTCGC TGGCCTTGCC CTGGAATAA 780
 GGAGCCTCTA GCATGGGCCC TGCATGCTAA TAAATGCTTC TTCAGAAAAA AAAAAAAAAA 840
 20 AACTCGAGG GGGGCCCGGT ACCCA 865

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2082 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

TGGGGGGGN AATGGGTGTC TGGCTCANGG ATTGCCNAAT CTGGAAATTC TCCATAACTT 60
 35 GCTAGCTTGT TTTTTTTTTT TTTTTTTTACA CCCCCCGCC CCACCCCGG ACTTGACAA 120
 TGTCAATGA TCTCAGCAGA GTTCTTCATG TGAAACGTTG ATCACCTTTG AAGCCTGCAT 180
 40 CATTCACATA TTTTTTCTTC TTCTTCCCT TCAGTTCATG AACTGGTGTT CATTTTCTGT 240
 GTGTGTGTGT GTTTATTTTT GTTTGGATTT TTTTTTTTAA TTTTACTTTT AGAGCTTGCT 300
 GTGTGCCCCA CCTTTTPTCC AACCTCCACC CTCACTCCTT CTCAACCCAT CTCTTCCGAG 360
 45 ATGAAAGAAA AAAAAAGCA AAGTTTTTTT TTCTTCTCCT GAGTTCTTCA TGTGAGATTG 420
 AGCTTGCAA GGAAAAAAAA ATGTGAAATG TTATAGACTT GCAGCGTGCC GAGTTCCATC 480
 50 GGGTTTTTTT TTATGCTATG TTATGCTAAA ATAGAGAAAA AAATGCTCAT GAACCTTCCA 540
 CAATCAAGCC TGCATCAACC TTCTGGGTGT GACTTGTGAG TTTTGGCCTT GTGATGCCAA 600
 ATCTGAGAGT TTAGTCTGCC ATTAAAAAAA CTCATTCTCA TCTCATGCAT TATTATGCTT 660
 55 GCTACTTTGT CTAGCAACA ATGAACTATA ACTGTTTCAA AGACTTTATG GAAAAGAGAC 720
 ATTATATTAA TAAAAAAA AAGCCTGCAT GCTGGACATG TATGGTATAA TTATTTTTTC 780
 60 CTTTTTTTTT CCTTTTGGCT TGAAATGGA CGTTCGAAGA CTTATAGCAT GGCATTCATA 840

5 CTTTGTGTTT ATTGCCTCAT GACTTTTGTG AGTTTAGAAC AAAACAGTGC AACCGTAGAG 900
 CCTTCTTCCC ATGAAATTTT GCATCTGCTC CAAAACTGCT TTGAGTTACT CAGAACTTCA 960
 ACCTCCCAAT GCACTGAAGG CATTCTTGTG GCAAAGATAC CAGAAATGGG TACACATTTA 1020
 ACCTGGCAAA CATTGAAGAA CTCTTTRATGT TTTCTTTTTA ATAAGAATGA CGCCCCACTT 1080
 10 TGGGGACTAA AATTGTGCTA TTGCCGAGAA GCAGTCTAAA ATTTATTTTT TAAAAAGAGA 1140
 AACTGCCCCA TTATTTTGGG TTTGTTTTAT TTTTATTTTA TATTTTGGG CTTTGGTCA 1200
 TTGTCAAATG TGGAATGCTC TGGGTTTCTA GTATATAATT TAATCTAGT TTTTATAATC 1260
 15 TGTTAGCCCA GTTAAATGT ATGCTACAGA TAAAGGAATG TTATAGATAA ATTTGAAAGA 1320
 GTTAGGTCTG TTTAGCTGTA GATTTTAA ACGATTGATG CACTAAATG TTTACTATTG 1380
 20 TCATGTTAAG GGGGTAGAG TTTGCAAGGG GACTGTTTAA AAAAGTAGC TTATACAGCA 1440
 TGTGCTTCCA ACTTAAATAT AAGTTGGGTA TGTGTAGTCT TTGCTATACC ACTGACTGTA 1500
 TTGAAAACCA AAGTATTAAG AGGGGAAACG CCCCTGTTTA TATCTGTAGG GGTATTTTAC 1560
 25 ATTCAAAAAT GTATGTTTTT TTTCTTTTC AAAATTAAAG TATTTGGGAC TGAATTGCAC 1620
 TAAGATATAA CCTGCAAGCA TATAATACAA AAAAAAATTG CAAAAGTGT TAGAACGCTA 1680
 30 ATAAATTTTA TGCAGTTATA AAAATGGCAT TACTGCACAG TTTTAAGATG ATGCAGATTT 1740
 TTTTACAGTT GTATTGTGGT GCAGAACTGG ATTTCTGTGTA ACTTAAAAA AAATCCACAG 1800
 TTTTAAAGGC AATAATCAGT AAATGTTATT TTCAGGACT GACATCCTGT CTTTAAAAAG 1860
 35 AAATGAAAAG TAAATCTTAC CACAATAAAT ATAAAAAAT CTTGTCAGTT ACTTTTCTTT 1920
 TACATATTTT GCTGTGCAAA ATTGTTTTAT ATCTTGAGTT ACTAACTAAC CACGCGTGT 1980
 40 GTTCCTATGT GCTTTTCTTT CATTTTCAAT TCTGGTTATA TCAAGAAAAG AATAATCTAC 2040
 AATAATAAAC GGCATTTTTT TTTGAAAAA AAAAAAAAAA AA 2082

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(2) INFORMATION FOR SEQ ID NO: 252:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

CAGGCAGGCT GGCCCCGGG ACTTCTCTCT GGCCCTGCTC CCTCCGAGCG CTCCGCCGTT 60
 GCGCCCTGG CCCCTACGGA GTCCTTAGCC AGGATGGAGG CTGTTGTGAA CTTGTACCAA 120

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GAGGTGATGA AGCACGCAGA TCCCCGATC CAGGGCTACC CTCTGATGGG GTCCCCCTTG 180
 CTAATGACCT CCAATCTCCT GACCTACGTG TACTTCGTTC TCTCACTTGG GCCTCGCATC 240
 5 ATGGCTAATC GGAAGCCCTT CCAGCTCCGT GGCTTCATGA TTGTCTACAA CTCTCACTG 300
 GTGGCACTCT CCCTCTACAT TGTCTATGAG TTCTGATGT CGGGCTGGCT GAGCACCTAT 360
 ACCTGGCGCT GTGACCCTGT GGACTATTCC AACAGCCCTG AGGCACCTAG GATGGTTCGG 420
 10 GTGGCCTGGC TCTTCCTCTT CTCCAAGTTC ATTGAGCTGA TGGACACAGT GATCTTTATT 480
 CTCCGAAAGA AAGACGGGCA GGTGACCTTC CTACATGTCT TCCATCACTC TGTGCTTCCC 540
 15 TGGAGCTGGT GGTGGGGGGT AAAGATTGCC CCGGGAGGAA TGGGCTCTTT CCATGCCATG 600
 ATAAACTCTT CCGTGCATGT CATAATGTAC CTGTACTACG GATTATCTGC CTTTGGCCCT 660
 GTGGCACAAC CCTACCTTTG GTGGAAAAAG CACATGACAG CCATTCAGCT GATCCAGTTT 720
 20 GTCTCTGGTCT CACTGCACAT CTCCCAGTAC TACTTTATGT CCAGCTGTAA CTACCAGTAC 780
 CCAGTCATTA TTCACCTCAT CTGGATGTAT GGCACCATCT TCTTCATGCT GTTCTCCAAC 840
 25 TTCTGGTATC ACTCTTATAC CAAGGGCAAG CGGCTGCCCC GTGCACTTCA GCAAAATGGA 900
 GCTCCAGGTA TTGCCAAGGT CAAGGCCAAC TGAGAAGCAT GGCCTAGATA GGGCCCCACC 960
 TAAGTGCCCTC AGGACTGCAC CTTAGGGCAG TGTCCGTCAG TGCCCTCTCC ACCTACACCT 1020
 30 GTGACCAAGG CTTATGTGGT CAGGACTGAG CAGGGGACTG GCCCTCCCCT CCCACAGCT 1080
 GCTCTACAGG GACCACGGCT TTGGTTCCTC ACCCACTTCC CCGGGCAGC TCCAGGGATG 1140
 35 TGGCCTCATT GCTGTCTGCC ACTCCAGAGC TGGGGGCTAA AAGGGCTGTA CAGTTATTTC 1200
 CCCCTCCCTG CCTTAAACT TGGGAGAGGA GCACTCAGGG CTGGCCCCAC AAAGGGTCTC 1260
 GTGGCCTTTT TCCTCACACA GAAGAGGTCA GCAATAATGT CACTGTGGAC CCAGTCTCAC 1320
 40 TCCTCCACCC CACACACTGA AGCAGTAGCT TCTGGGCCAA AGGTCAGGGT GGGCGGGGGC 1380
 CTGGGAATAC AGCCTGTGGA GGCTGCTTAC TCAACTTGTG TCTTAATTAA AAGTGACAGA 1440
 45 GGAAACCAAA AAAAAAAAAA AAAAACTCGA GGGGGGCCCC TA 1482

50 (2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

60 GGCACGAGCG CCGTGGCCCG CCTGGCCCCT ACGGAGTCCT TAGCCAGGAT GGAGGCTGTT 60

5 GTGAACCTTGT ACCAAGAGGT GATGAAGCAC GCAGATCCCC GGATCCAGGG CTACCCCTCTG 120
 ATGGGGTCCC CCTTGCTAAT GACCTCCATT CTCCTGACCT ACGTGTACTT CGTTCTCTCA 180
 CTTGGGCCTC GCATCATGGC TAATCGGAAG CCCTTCCAGC TCCGTGGCCT CATGATTGTC 240
 TACAACTTCT CACTGGTGGC ACTCTCCCTC TACATTGTCT ATGAGTTCCT GATGTCGGGC 300
 10 TGGCTGAGCA CCTATACCTG GCGCTGTGAC CCTCAGGACT GCACCTTAGG GCAGTGTCCG 360
 TCAGTCCCCT CTCCAMCTAC ACCTGTGACC AAGGCTTATG TGGTCAGGAC TGAGCAGGGG 420
 ACTGGCCCTC CCTTCCCCAC AGCTGCTCTA CAGGGACCAC GGCTTTGGTT CCTCACCAC 480
 15 TTCCCCGGG CAGCTCCAGG GATGTGGCCT CATTGCTGTC TGCCACTCCA GAGCTGGGG 540
 CTAAGAGGGC TGTACAGTTA TTTCCCCCTC CCTGCCTTAA AACTTGGGAG AGGAGCACTC 600
 20 AGGGCTGGCC CCACAAAGGG TCTCGTGGCC TTTTCTCTCA CACAGAAGAG GTCAGCAATA 660
 ATGTCACTGT GGACCCAGTC TCACTCCTCC ACCCCACACA CTGAAGCAGT AGCTTCTGGG 720
 CCAAAGGTCA GGGTGGGCGG GGGCCTGGGA ATACAGCCTG TGGAGGCTGC TTACTCAACT 780
 25 TGTGTCTTAA TTAAAAGTGA CAGAGGAAAC CACGAAAAA AAAAAAAAAA AAAA 834

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(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

TTGAACCTTTT AAAATTTTAG ATCAGCAAAC TCTAAGATCC TAGAATGGAA GCTGTTCTCTC 60
 ATTTCTCCAT GCTCACCCTC CCAGGTCAGC GAGATGGTGA AGAAGCTGCA CGCGGCAACA 120
 45 CCACCAACGT TCGGAGTGGG CCTCATCAAT GAGCTTGTGG AGAACTTTGG CAGATGTCCC 180
 AAGTGGTCTG GTCGGCAAGC CTTTGTCTTT GTCTGCCAGA CTCTCATTGA GGATGACTGC 240
 CTTCCCATGG ACCAGTTTGC TGTGCATCTC ATGCCGCATC TGCTAACCTT AGCAAATGAC 300
 50 AGGGTTCTTA ACGTGGAGT GCTGCTTGCA AAGACATTAA GACAACTCT ACTAGAAAAA 360
 GACTATTTCT TGGCCTCTGC CAGCTGCCAC CAGGAGGCTG TGGAGCAGAC CATCATGGCT 420
 55 CTTCAGATGG ACCGTGACAG CGATGTCAAG TATTTTGCAA GCATCCACCC TGCCAGTACC 480
 AAAATCTCCG AAGATGCCAT GAGCACAGCG TCCTCAACCT ACTAGAAGGC TTGAATCTCG 540
 60 TGCTCTTTCC TGCTTCCATG AGAGCCGAGG TTCAGTGGGC ATTCGCCACG CATGTGACCT 600

	GOGATAGCTT TCGGGGGAGG AGAGACCTTC CTCCTCTGCG GACTTCATTG CAGGTGCAAG	660
	TTGCCTACAC CCAATACCAG GGATTTCAG AGTCAAGAGA AAGTACAGTA AACACTATTA	720
5	TCTTATCTTG ACTTTAAGGG GAAATAATTT CTCAGAGGAT TATAATTGTC ACCGAAGCCT	780
	TAAATCCTTC TGTCTTCCTG ACTGAATGAA ACTTGAATTG GCAGAGCATT TTCCTTATGG	840
10	AAGGGATGAG ATTCCCAGAG ACCTGCATTG CTTTCTCCTG GTTTTATTTA ACAATCGACA	900
	AATGAAATTC TTACAGCCTG AAGGCAGACG TGTGCCCAGA TGTGAAAGAG ACCTTCAGTA	960
	TCAGCCCTAA CTCTTCTCTC CCAGGAAGGA CTTGCTGGGC TCTGTGGCCA GCTGTCCAGC	1020
15	CCAGCCCTGT GTGTGAATCG TTTGTGACGT GTGCAAATGG GAAAGGAGGG GTTTTACAT	1080
	CTCTTAAAGG ACCTGATGCC AACACAAGTA GGATTGACTT AACTCTTAA GCGCAGCATA	1140
20	TTGCTGTACA CATTTACAGA ATGGTGTCTG AGTGTCTGTG TCTGATTTTT TCATGCTGGT	1200
	CATGACCTGA AGGAAATTTA TTAGACGTAT AATGTATGTC TGGTGTTTTT AACTTGATCA	1260
	TGATCAGCTC TGAGGTGCAA CTTCTTCACA TACTGTACAT ACCTGTGACC ACTCTTGGGA	1320
25	GTGCTGCAGT CTTTAATCAT GCTGTTTAAA CTGTTGTGGC ACAAGTTCTC TTGTCCAAAT	1380
	AAAATTTATT AATAAGATCT ATAGAGAGAG ATATATACAC TTTTGATTGT TTTCTAGATG	1440
30	TCTACCAATA AATGCAATTT GTGACCTGTA TTAATAAAAA NTAAAAAAC TCGAGGGGGG	1500
	CCCGGTAC	1508

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(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2514 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

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	GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGGAAGA	60
	GCACCTACCT GTGTTGGTGA GGTTTGTTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT	120
50	AGGCTTCCTG CCTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTTT ACACATATGAT	180
	AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCGTGGC CAGGCTTACA TTGWCTCTAG	240
	TGGATTTTCT TCCAAAATGA AAGTTGTTGC TTCTAGACTT TTAGAGAAAT ATCCCCAAGC	300
55	TATCTACACA CTCTGCTCTT CCTGTGCCTT AAATATGTGG TTGGCAAAAT CAGTACCTGT	360
	TATGGGAGTA TCTGTTGCAT TAGGAACAAT TGAGGAAGTT TGTTCCTTTT TCCATCGATC	420
60	ACCACAACCTG CTTTATAGAAC TTGACAACGT AATTTCGTGT CTTTTCAGTA ACAGTAAAGA	480

	AAGGGGTAAA GAACTGAAGG AAATCTGCCA TTCTCAGTGG ACAGGCAGGC ATGATGCTTT	540
5	TGAAATTTTA GTGGAAGCTC TGCAAGCACT TGTTTTATGT TTAGATGGTA TAAATAGTGA	600
	CACAAATATT AGATGGAATA ACTATATAGC TGGCCGAGCA TTTGTACTCT GCAGTGCAGT	660
	GTCAGATTTT GATTTCAATTG TTACTATTGT TGTCTTAAA AATGTCCTAT CTTTACAAG	720
10	AGCCTTTGGG AAAAACCTCC AGGGGCAAAC CTCTGATGTC TTCTTTGCGG CCGGTAGCTT	780
	GACTGCAGTA CTGCATTAC TCAACGAAGT GATTGGAAAA TATTGAAGTT TATCATGAAT	840
15	TTTGGTTTGA GGAAGCCACA AATTTGGCAA CCAAAGTTGA TATTCAAATG AAAGTCCCTG	900
	GGAAATTCAG CAGAGCTCAC CAGGGTAACT TGGAATCTCA GCTAACCTCT GAGAGTTACT	960
	ATAAAGAAAC CCTAAGTGT CCAACAGTGG AGCACATTAT TCAGGAAGTT AAAGATATAT	1020
20	TCTCAGAACA GCACCTCAA GCTCTTAAAT GCTTATCTCT GGTACCTCA GTCATGGGAC	1080
	AACTCAAAT CAATACGTCG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA	1140
25	ATCTGACAC GCTGTCAGCT GAGCTTCATT GTTGGAGAAT CAAATGGAAA CACAGGGGGA	1200
	AAGATATAGA GCTTCCGTCC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTTT	1260
	TTCTAATGT GATGCATTG CTGAAGGTCC TGTGTATTCT TCCTGTGATG AAGTTGAGA	1320
30	ATGAGCGGTA TGAAATGGA CGAAAGCGTC TTAAAGCATA TTTGAGGAAC ACTTTGACAG	1380
	ACCAAAGGTC AAGTAACTTG GCTTTGCTTA ACATAAATTT TGATATAAAA CACGACCTGG	1440
35	ATTTAATGGT GGACACATAT ATTAACTCT ATACAAGTAA GTCAGAGCTT CCTACAGATA	1500
	ATTCGAAAC TGTGGAAAAT ACCTAAGAGA CTTTTAAAA TAGGCTTTCT TATATTGAT	1560
	ATTTGAAGA AAAAGCCGTA AGTGTATGTA GACCACCTAA TCACTAAATA TCTTTGCCTA	1620
40	TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTTAAATGG CCCCTGTTTG	1680
	AACTCTCAAG CTTTGAAGAC CTACCTGTTT TTCCAGAAGA GAACGTTGAA AGTGCCATGT	1740
45	TTCTTTTGC GTGATCTCTG TTGATGGCAC TCTGGAATG TTTCAAGTAA GTCATTTTAG	1800
	ACATAGCATT TATTATCACT GTGGATCTCT ACTTGTGGG TGTATGAAT TCTTTGAAGA	1860
	AATATATTTT GAAGAGGTGT GGGAGGAAG AATACATTTT ATAAATGTT GTAGTGAAGC	1920
50	CCACAATTGA CCTTGAAGTA ATAGGAGTTT TAAGTATGTT AAAATCTAT ACTGGACAGT	1980
	TACAAGAAAT TACCGAGAA AAGCTTGTGA GCTACCAAA CAAGGATTTT AGTGTAGATT	2040
55	TTGTCTTTCT TGAAGTTAAA GAAACAAATG ACAAAGTTTG AATGGAAAAG CCTGCTGTTG	2100
	TTCCACATCT CGTTGCTGTT TACATTCTTT TGTGGAGCCT ACATCTTCTT AAGCTTTTAA	2160
	GCAGGTATAT GTTGAACACT TCTGTTTCAT GGTGAGACA GAATCAGAGG CCATGGATAC	2220
60	TGACAACTGA TTTGTCTGTT TTTTCTCTCT GTCCTTTTCC ATGACTCTTA TATACTGCCT	2280

CATCTTGATT TATAAGCAAA ACCTGGAAAA CCTACAAAAT AAGTGTGTG GTTTATCTAG 2340
 5 AAAAATATGG AAAATATTGC TGTATTMTT GGTGAAGAAA ATCAATTTTG TATAGTTTAT 2400
 TTCAATCTAA ATAAAATGTG AATTTTGT TT AAAGCTTAGG CACATTATTT TTTGTGGGGT 2460
 CAAAACATTC TTGTGTAAAT TCTCTTAAAC ATTTGATAAA CAGCTTCACA ATTC 2514
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(2) INFORMATION FOR SEQ ID NO: 256:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

CTGCCITTATG AAGCCGATGC AGAAATTTTG GCTGTGAAAT TTCACACTAT GATAACTGAG 60
 25 AAGTGGGGAT TAAATATGGA GTATTGTCGT GGCCAGGCTT ACATTGTCTC TAGTGGATTT 120
 TCTTCCAAAA TGAAAGTTGT TGCTTCTAGA CTTTATAGAGA AATATCCCCA AGCTATCTAC 180
 ACACTCTGCT CTTCTGTGC CTAAATATG TGGTTGGCAA AATCAGTACC TGTTATGGGA 240
 30 GTATCTGTG CATTAGGAAC AATTGAGGAA GTTTGTCTT TTTTCCATCG ATCACCACAA 300
 CTGCTTTTAG AACTTGACAA CGTAATTYCT GTTCTTTTTC AGAACAGTAA AGAAAGGGGT 360
 35 AAAGAACTGA AGGAAATCTG CCATTCTCAG TGGACAGGCA GGCATGATGC TTTTGAAATT 420
 TTAGTGAAC TCCTGCAAGC ACTTGTTT TA TGTATTAGATG GTATAAATAG TGACACAAAT 480
 ATTAGATGGA ATAACTATAT AGCTGGCCGA GCATTTGTAC TCTGCAGTGC AGTGTGAGAT 540
 40 TTTGATTCA TTGTTACTAT TGTGTCTT AAAAATGTCC TATCTTTTAC AAGAGCCTTT 600
 GGGAAAAACC TCCAGGGGCA AACCTCTGAT GTCTTCTTTG CGGCCGGTAG CTTGACTGCA 660
 45 GTACTGCATT CACTCAACGA AGTGANTGGA AAATATTGAA GTTTATCATG AATTTTGGTT 720
 TGAGGAAGCC ACAAATTTGG CAACCAAACT TGATATTCAA ATGAAACTCC CTGGGAAATT 780
 CCGCAGAGCT CACCAGGTA ACTTGGAATC TCAGCTAACC TCTGAGAGTT ACTATAAAGA 840
 50 AACCCTAAGT GTCCCAACAG TGGAGCACAT TATTGAGGAA CTAAAGATA TATTCTCAGA 900
 ACAGCACCTC AAAGCTCTTA AATGCTTATC TCTGGTACCC TCAGTCATGG GACAACTCAA 960
 55 ATTCAATACG TCGGAGGAAC ACCATGCTGA CATGTATAGA AGTGACTTAC CCAATCCTGA 1020
 CACGCTGTCA GCTGAGCTTC ATTTGTTGGAG AATCAAATGG AAACACAGGG GGAAAGATAT 1080
 AGAGCTTCCG TCCACCATCT ATGAAGCCCT CCACCTGCCT GACATCAAGT TTTTTCCTAA 1140
 60

	TGTGTATGCA TTGCTGAAGG TCCTGTGTAT TCTTCCTGTG ATGAAGGTTG AGAATGAGCG	1200
	GTATGAAAAT GGACGAAAGC GTCTTAAAGC ATATTTGAGG AACACTTTGA CAGACCAAAG	1260
5	GTCAAGTAAC TTGGCTTTGC TTAACATAAA TTTTGATATA AAACACGACC TGGATTTAAT	1320
	GGTGGACACA TATATTAAAC TCTATACAAG TAAGTCAGAG CTTCTACAG ATAATCCGA	1380
10	AACTGTGGAA AATACCTAAG AGACTTTTAA AAATAGGCTT TCTTATATTT GATATTTGGA	1440
	AGAAAAAGCC GTAAGTGTAT GTAGACCACT TAATCACTAA ATATCTTTGC CTATAGGACT	1500
	CCATTGAATA CATTAGCCAT TGATAATCTA CCTGTTTAAA TGGCCCTGT TTGAACTCTC	1560
15	AAGCTTTGAA GACCTACCTG TTCTTCCAGA AGAGAACGTT GAAAGTGCCA TGTTCCTTT	1620
	TGCGTGATCT CTGTTGATGG CACTCTGGAA TTGTTTCAGT TAAGTCATTT TAGACATAGC	1680
20	ATTTATATC ACTGTGGATC TCTACTTGT GGGTGTATG AATCTTTGA AGAAATATAT	1740
	TTTGAAGAGG TGTGGGAGGA AGGAATACAT TTTATAAAAT GTTGTAGTGA AGCCACAAT	1800
	TGACCTTTGA CTAATAGGAG TTTTAAGTAT GTTAAAAATC TATACTGGAC AGTTACAAGA	1860
25	AATTACCGGA GAAAAGCTTG TGAGCTCACC AAACAAGGAT TTCAGTGTAG ATTTTGTCTT	1920
	TCTTGAACCT AAAGAAACAA ATGACAAAGT TTGAATGGAA AAGCCTGCTG TTGTTCCACA	1980
30	TCTCGTTGCT GTTTACATTC CTTTGTGGAG CCTACATCTT CCTAAGCTTT TTAGCAGGTA	2040
	TATGTTGAAC ACTTCTGTTT CATGGTTGAG ACAGAATCAG AGGCCATGGA TACTGACAAC	2100
	TGATTTGTCT GTTTTTTTTC TCTGTCTTTT TCCATGACTC TTATATACTG CCTCATCTTG	2160
35	ATTTATAAGC AAAACCTGGA AAACCTACAA AATAAGTGTT GTGGTTTATC TAGAAAAATA	2220
	TGGAATAATAT TGCTGTTATT TTTGGTGAAG AAAATCAATT TTGTATAGTT TATTTCAATC	2280
40	TAAATAAAAT GTGAATTTTG TTTAAAGCTT AGGCACATTA TTTTTTGTGG GGTCAAAACA	2340
	TTCTTGTGTA AATTCTC	2357

45

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

	ACTTTCCTGGT GCAAAAAGAT GTTCAAGCCT TATTTTATAC TTGCCTGCCC CTTTCTCTTT	60
	CATTTATTGG AGTGAGCTGC AGCTCTAAGA AGACCTGTTC TTTTGAATGG AGAGTAGCAT	120
60	CAGGAACCAG GATGTGGGTG CGAGGCGTGC TCCTGGCTGT TGCAGATTGC TGCACCGGG	180

AGCTCTTAGT GGACAGAGCT AGAGGATATG TGCACGTA CTCCATCTCTC TCTCTGTCTC 240
 CGATTTTAGC CCAGCACCAC AGGGTACGTT CCAGTTTTTC TCTCTTTCCA TAGCTGTAAG 300
 5 GCCCTTTCTG GGAATGGTTC TCATTCTCCT TAATCTATTA TTGGGTCAGT TTTCCTGCAT 360
 GTCCCCAGCC TCCCATCACT GCCACCCACT CCCCACAGAG ATGCCCTGCT CATCCGACTG 420
 10 GGGCTTTGAC TCCCACACTG TGTACCCCTC TTGTGTGGAC GCCCTGCTGC CAAAACCTTC 480
 AGCAAACAGC TTTCCAAATG GAAGTTGTCA CTGTCAAGGS CTTTACAATC AGCAACAGCA 540
 AAATCTACAT GCTGCTGAGG GTCCTGCCTC ATTAAGATGC AATAAATATG TAAGTACATA 600
 15 AAAACAGCAA TAGAAGAAAC GTAATGCTTT ATTCTCAAAT ATGNATGTCT ACATAGAAAA 660
 GCCAAAATTA TTAAGAATAG TAAGGAATT 689
 20

(2) INFORMATION FOR SEQ ID NO: 258:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

TCGACCCACG CGTCCGCCGA TGTGATGATT CCTGCGTATT CCAAGAACCG GGCCTATGCC 60
 35 ATCTTCTTCA TAGTCTTAC TGTGATAGGG GAGCCCCCG GCGCTGTGCT ATCCTGTGCC 120
 GGCCACCTT GCGTGGTTT TGCTGTGTA CTGGTGGCG CCCTGACCGT GGCTGTCTCC 180
 TCTTGAAGGA AGCCTGTTTC TGATGAACCT GCTGACAGCC ATCATCTACA GTCAGTTCCG 240
 40 GGGCTACCTG ATGAAATCTC TCCAGACCTC GCTGTTTCGG AGGCGGGTGG GAACCCGGCT 300
 GCCTTTGAAG TCCTATCCTC CATGGTGGG GAGGGAGGAG CCTTCCCTCA GGCAGTTGGG 360
 45 GTGAAGCCCC AGAAGTTGCT GCAAGTGCTT CAGAAGGTCC AGCTGGACAG CTCCCACAGA 420
 CAGGCCATGA TGGAGAAGGT GCGTTCCTAT GGCAGTGTTG TGCTCTCAGC TGAGGAGTTT 480
 CAGAAGCTCT TCAACGAGCT TGACAGAAGT GTGGTTAAAG AGCACC CGC GAGGCCGAG 540
 50 TACCACTCTC CGTTTCTGCA GAGCGNCCCA GTTCTCTTTC GGCCACTNAC TACTTTGACT 600
 ACCTGGGGAA CCTCATCGCC CTGGCAAACC TGGTGCCAT TTGCGTGTTC CTGGTGCTGG 660
 55 ATGCAGATGT TGCTGCCTGC TGAGCGTGAT GACTTCATCC TGGGGGGTCT CAACTGCGTC 720
 TTCATTGTGT ACTACCTGTT GGAGATGCTG GCTCAAGGTC TTTTGCCCTG GGCCTGCGA 780
 RGGTACYKKT CCTAACCCCA RCAAMGTGTT TTGAACGGGC TCCTCAMCGT TTGTCTGGC 840
 60

TGGWWKKGSM GATCTCAACT CTGGCTGTGT ACCGATTGCC ACACCCAGGC TGGAGGCCGG 900
 ANATGGTGGG CCTGCTGTCTG CTGTGGGACA TGACCCGCAT ACTGAACATG CTCATCGTGT 960
 5 TCCGCTTCCT GCGTATCATC CCCAGCATGA AGCCGATGGC CGTGGTGGCC AGTACCGTCC 1020
 TGGGCCTGGT GCAAAACATG CGTGCGTTTG GCGGGATCCT GGTGGTGGTC TACTACGTAT 1080
 10 TTGCCATCAT TGGGATCAAC TTGTTTAGAG GCGTCATGT GGCTCTTCCT GGAAACAGCA 1140
 GCCTGGCCCC TGCCAATAGG TCGGCGCCCT GTGGGAGCTT CGAGCAGCTG GAGTACTGGG 1200
 CCAACAACCTT CGATGACTTT GCGGCTGCCC TGGTCACTCT GTGGAACCTG ATGGTGGTGA 1260
 15 ACAACTGGCA GGTGTTTCTG GATGCATATC GCGCTACTA AGGCCCGTGG TCCAAGATCT 1320
 ATTTTGTATT GTGGTGGCTG GTGTCTCTG TCATCTGGGT CAACCTGTTT CTGGCCCTGA 1380
 TTCTGGAGAA CTTCCTTCAC AAGTGGGACC CCCGAGCCA CCGCAGCCC CTGCTGGGA 1440
 20 CCCCAGAGGC CACCTACCG ATGACTGTGG AGCTCCTGTT CAGGGATATT CTGGAGGAGC 1500
 CCGGGGAGGA TGAGCTCACA GAGAGGCTGA GCCAGCACC GCACCTGTGG CTGTGCAGGT 1560
 25 GACGTCCGG TCTGCCATCC CAGCAGGGG GGCAGGAGAG AGAGGCTGGC ATAACACAGG 1620
 TGCCCATCAT GGAAGAGGCG GCCATGCTGT GCCAGCCAG GCAGGAAGAG ACCTTTCCTC 1680
 TGACGGACCA CTAAGCTGGG GACAGGAACC AAGTCCTTTG CGTGTGGCCC AACACCATT 1740
 30 TACAGAACAG CTGCTGGTGC TTCAGGGAGG CGCCGTGCCC TCCGCTTTCT TTTATAGCTG 1800
 CTTCAGTGAG AATTCCTTG TCGACTCCAC AGGGACCTTT CAGACAAAA TGCAAGAAGC 1860
 35 AGCGGCCTCC CCGTCCCTT GCAGCTTCCG TGGTGCCTTT GCTGCCGGCA GCCCTTGGGG 1920
 ACCACAGGCC TGACCAGGC CTGCACAGGT TAACCGTCAG ACTTCCGGG CATTCAGCTG 1980
 GGAATGATAC TAATACCTCC GATTTTAGCC CAGCACCACA GGTACGTTT CAGTTTATTAT 2040
 40 TTCTTTCCAT AGCTGTAAGG CCTTTCTGG GAATGTTTAT CATTCCTTT AATCTATTAT 2100
 TGGGTCAGTT TTCTGCATG TCCCAGCCT CCCATCACTG CCACCCACTC CCCACAGAGA 2160
 45 TGCCCTGCTC ATCCGACTGG GGCTTTGACT CCCACACTGT GTACCCCTCT TGTGTGGACG 2220
 CCTGCTGCC AAAACCTTCA GCAAACAGCT TTCCAAATGG AAGTTGTAC TGTGAGGGC 2280
 TITACAATCA GCAACAGCAA AATCTACATG CTGCTGAGGG TCCTGCTCA TTAAGATGCA 2340
 50 ATAAATATGT AAGTACATAA AAAAAAAAAA AAAAAA 2377

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(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1193 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

5 TCTGNTCGCC GTCGCCCCGC CCTGGCCTT TGCCCGGTG GCGGGGACTT CCTGTGTGCT 60
ATTTCCAAGG ACTCCAAGC GAGGCCGGG ACTGAAGGTG TGGGTGTGCA GCCCTCTGGC 120
10 AGAGGGTTAA CCTGGGTCAA ATGCACGGAT TCTCACCTCG TACAGTTACG CTCTCCCGG 180
GCACGTCCGC GAGGMYTTGA AGTCTGAGC GCTCAAGTTT GTCCGTAGTC GAGAGAAGGC 240
CATGGAGGTG CCGCCACCGG CACCGCGGAG CTTTCTCTGT AGAGCATTGT GCCTATTTCC 300
15 CCGAGTCTTT GCTGCCGAAG CTGTGACTGC CGATTGCGAA GTCCTTGAGG AGCGTCAGAA 360
GCGGCTTCCC TACGTCCAG AGCCCTATTA CCGGAATCT GGATGGGACC GCCTCCGGGA 420
20 GCTGTTTGGC AAAGACACAG TGAACACTAG TCTGAATGTA TACCGAAATA AAGATGCCTT 480
AAGCCATTTT GTAATTGCAG GAGCTGTCAC GGAAGTCTT TTTAGGATAA ACGTAGGCCT 540
GCGTGGCTGG TGGCTGGTGG CATAATGGA GCCTTGCTGG GCACTCCTGT AGGAGGCCTG 600
25 CTGATGGCAT TTCAGAAGTA CTCTGGTGAG ACTGTTGAGG AAAGAAAACA GAAGGATCGA 660
AAGGCACTCC ATGAGCTAAA ACTGGAAGAG TGGAAAGGCA GACTACAAGT TACTGAGCAC 720
30 CTCCTGAGA AAATTGAAAG TAGTTTACAG GAAGATGAAC CTGAGAATGA TGCTAAGAAA 780
ATTGAAGCAC TGCTAAACCT TCCTAGAAAC CCTTCAGTAA TAGATAAACA AGACAAGGAC 840
TGAAAGTGCT CTGAACTTGA AACTCACTGG AGAGCTGAAG GGAGCTGCCA TGTCCGATGA 900
35 ATGCCAACAG ACAGGCCACT CTTTGGTCAG CTGCTGACA AATTTAAGTG CTGGTACCTG 960
TGGTGGCAGT GGCTTGCTCT TGTCCTTTTC TTTTCTTTTT AACTAAGAAT GGGGCTGTTG 1020
40 TACTCTCACT TTAATTATCC TTAATTTAA ATACATACTT ATGTTTGTAT TAATCTATCA 1080
ATATATGCAT ACATGAATAT ATCCACCCAC CTAGATTTTA AGCAGTAAAT AAAACATTTT 1140
GCAAAAGATT AAAGTTGAAT TTTACAGTTA AAAAAAAAAA AAAAAAAAAA AAA 1193
45

(2) INFORMATION FOR SEQ ID NO: 260:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

60

GA AAAACCCA AAGATGCAGA CAATCTCTTT GAACATGAAT TGGGGGCTCT CAATATGGCT 60

	GCATTACTAC	GAAAAGAAGA	AAGAGCAAGT	CTTCTTAGTA	ATCTTGCCCC	ATGTTGTAAG	120
	GCGTTGTGCT	TCAGACGGGA	TTCGCAATT	CGAAAGCAGC	TTGTTAAAAA	TGAGAAGGGC	180
5	ACCATAAAAC	AAGCTTACAC	GAGTSCCTCA	ATGGTAGACA	ATGAATTACT	TCGATTGAGT	240
	CTTCGGTTAT	TTAAGCGGAA	GACTACTTGC	CATGCTCCAG	GACATGAAAA	GACTGAAGAT	300
	AATAAACTTT	CACAGTCCAG	TATCCAACAG	GAAGTGTGTG	TGTCTTAAGA	CCGAAGTTCA	360
10	ATATGGTATT	TTTGGTACTG	TCTTCCTTCA	GCAGTGCATA	TTCTTTTGCA	AAGTCTTTTG	420
	GTTTGACAAG	CATTAGTGAC	AAAGGCAGAA	AAGATTTATC	AGCCATGCTA	AAAGAGTGAA	480
15	GAATTTTGAT	CTTTAGAGAC	ACTAGTTTTG	GCCAACTTAA	GATTTTACGT	TAATTTTTTAC	540
	ATAGTATTTG	ACACTCATGC	AAAATAATGT	GAAAACATCT	AGATTTAGTA	GTTTATTCTG	600
	CGCCTTTTGT	TAAAACTGAA	GATTTTGGAA	AATGGTTGTC	ACTGCTCTTC	CAGCCTATGA	660
20	ATATTTTGT	GAAATGGAAC	CATGGATTTA	TGTCTGGATC	ATCCATACAG	AACCAACAAT	720
	TTTATTCAAA	AACAATGTGT	TCATCAAAGT	AATTGCTCAC	ATTGTGCAGT	ACTATGTTGT	780
25	ACAGACCACG	TGAAAGGGAA	TGCTGGTCTA	GCTGGCGTGG	TATGTTTATA	GGCGAATTTC	840
	AGCAGAAGGA	AGCCAAAATA	GTTTTTTCCT	TTTGAAAGTT	TTTTAAAAAT	TATTTTCATGG	900
	GTCTTTTMTT	TAATTAATAT	GTGTGCATTG	TTACAATGTA	TGTTGGATGT	CTTTTGACCC	960
30	TAAATGCTTT	TTTTGTATAT	AGAGATTGTG	TACTATTTTT	ATTTTAAATA	AATGTATCTT	1020
	CCCTTTCCTT	GTTTTAGATT	TACTTTGCTC	TTCGTTAATC	TTATTCCCTGA	TGATCTAGAA	1080
35	CATTAGTCAT	CAACATTACA	TGTTTCATGC	TTCAGATATT	TTACTGCTTG	TGTCCTTATT	1140
	GTTGGACAGC	TTTAAACAGA	GTTGATGGTA	CTTCAAATAT	AGCTCAATTGA	TACTTAAGGG	1200
	CANCTTCCCT	GGGATGTGGG	CTTTTTGGAA	GGAAAAAAT	TNCCCCAAAG	GCAAAATCCCA	1260
40	GT						1262

45

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

55

	GGCAAACCTT	CCCCAANGC	TTCGAAACTT	GCAAGCCGAA	ACCTTGAATC	GTTAAAAGTT	60
	GGGTTCGCNC	GGCGCCCTGG	CCCGAAGAAG	CGCAATTGGC	GTTCCGCGAA	CGTTGGCCCT	120
60	CAACGGCTCG	GCAGCCAGCC	ATGTCTTGCA	CCCAGGACAG	CGGCCCTGGG	CTACAAGGAC	180

CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA 240
 CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC 300
 5 ACCACTCACG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA 360
 CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTGTG 420
 10 GGATTCCCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTTCAAATCA AATTAGACTC 480
 TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCAATGACT GAGACATTTC ACCCCACAAT 540
 AATCGGGGAG AGCGTCTATG GCGATTTCCTA GGAAGCCTTT GATCACCTTT GTAACAAGAT 600
 15 CATTGCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAGT ACTGCAACCT 660
 CTTGGTGAGG GGCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG 720
 20 TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA 780
 TTTGCAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCTTCA 840
 TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA 900
 25 CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTG CTAATGTGGC 960
 TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA 1020
 30 CTACATTGCA CAGGTTTCAGC CAGTATTACG GTGCCAGCAA CAGACCTACT CCACTTGGCT 1080
 ACCCTGCAAT TAAGAATCAT TTAATAATGT CCTGTGGGA AGCCATTTC AACAAGACAG 1140
 GAGAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAGAGC 1179
 35

40 (2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

GGCAAACCTT CCCCCAANGC TTCGAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT 60
 50 GGGTTGCGNC GGCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT 120
 CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC 180
 55 CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA 240
 CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC 300
 ACCACTCACG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA 360
 60

CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTGTG 420
 GGATTCCTC CGGAGGCAGT TTGAATTGAG TGTAGATTCT TTTCAAATCA AATTAGACTC 480
 5 TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCCAATGACT GAGACATTTC ACCCCACAAT 540
 AATCGGGGAG AGCGTCTATG GCGATTTCCA GGAAGCCTTT GATCACCTTT GTAACAAGAT 600
 10 CATTCGCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAGT ACTGCAACCT 660
 CTTGGTGAGG GGCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG 720
 TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA 780
 15 TTTGCAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCTTCA 840
 TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA 900
 CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTG CTAATGTGGC 960
 20 TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA 1020
 CTACATTGCA CAGGTTGAGC CAGTATTACG GTGCCAGCAA CAGACCTACT CCACTTGGCT 1080
 25 ACCCTGCAAT TAAGAATCAT TTA AAAATGT CCTGTGGGA AGCCATTTCA GACAAGACAG 1140
 GAGAGAAAAA NAANGAAAAG AG 1162

30

(2) INFORMATION FOR SEQ ID NO: 263:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CCGGCTGGGT ATTTGCCTCG CACCATGGCG CCCAAGGGCA AAGTGGGCAC GAGAGGGAAG 60
 AAGCAGATAT TTGAAGAGAA CAGAGAGACT CTGAAGTTCT ACCTGCGGAT CATACTGGGG 120
 45 GCCAATGCCA TTTACTGCCT TGTGACGTTG GTCTTCTTTT ACTCATCTGC CTCATTTTGG 180
 GCCTGGTGG CCTTGGGCTT TAGTCTGGCA GTGTATGGG CCAGCTACCA CTCTATGAGC 240
 50 TCGATGGCAC GAGCAGCGTT CTCTGAGGA TGGGGCCCTG ATGGATGGTG GCACGAGCTC 300
 AACATGGAGC AGGGCATGGC AGAGCACCTT AAGGATGTGA TCCTACTGAC AGCCATCGTG 360
 CAGGTGCTCA GCTGCTCTC TCTCTATGTC TGGTCTTCT GGCTTCTGGC TCCAGGCCGG 420
 55 GCCCTTTACC TCCTGTGGGT GAATGTGCTG GGCCCTGGT TCACTGCAGA CAGTGGCACC 480
 CCAGCACCAG AGCACAATGA GAAACGGCAG CGCCGACAGG AGCGCGGCA GATGAAGCGG 540
 60 TTATAGCCAT TGACATTGTG GCCACAGGCC ACTGGCCCTG GGTGGCTCTG TCAGGGTGCA 600

5 CAGCCCCTCA TGCCTGGAGC AATGAGGGTC TAGTCCAGGG GCCAAAAGCA GTCTGAGGTA 660
TTGGGTATAC TTATACTCTA TAGGGTCGTT GAATAAATGG CTTAGAATGT GAAAAAAAAA 720
AAAAAAAAAA ATTTT 735

10

(2) INFORMATION FOR SEQ ID NO: 264:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AAGTGCATGA GCTGCCGATG TGGTGCTTAG TGATTGCGGT TTCGGTCGCT CTCCCGTGTT 60
TCCCGGGCTG GGTATTGCCC TCGCACCATG GCGCCCAAGG GCAAAGTGGG CACGAGAGGG 120
25 AAGAAGCAGA TATTTGAAGA GAACAGAGAG ACTCTGAAGT TCTACCTGCG GATCATACTG 180
GGGGCCAATG CCATTTACTG CCTTGTGACG TTGGTCTTCT TTTACTCATC TGCCTCATTT 240
TGGGCCTGGT TGGCCTGGGC TTTAGTCTGG CAGTGTATGG GGCCAGCTAC CACTCTATGA 300
30 GCTCGATGGC ACGAGCAGCG TTCTCTGAGG ATGGGGCCCT GATGGATGGT GGCATGGACC 360
TCAACATGGA GCAGGGCATG GCAGAGTGAG TGTCCCCAC CGCCAGCCCA GGCACCTTAA 420
35 GGATGTGATC CTA CTGACAG CCATCGTGCA GGIGCTCAGC TGCTTCTCTC TCTATGCTG 480
GTCTTCTGG CTTCTGGCTC CAGGCCGGGC CCTTTACCTC CTGTGGGTGA ATGTGCTGGG 540
CCCCTGTTT ACTGCAGACA GTGGCACCCC AGCACCAGAG CACAATGAGA AACGGCAGCG 600
40 CCGACAGGAG CGGCGGCAGA TGAAGCGGTT ATAGCCATG ACGATTTKGC SACNRGCCAC 660
TGGCCCTGGG TGGCTCTGTC AGGGTGCACA GCCCCTCATG CCTGGAGCAA TGAGGGTCTA 720
45 GTCCAGGGGC CAAAAGCAGT CTGAGGTATT GGGTATACTT ATACTCTATA GGGTCGTTGA 780
ATA 783

50

(2) INFORMATION FOR SEQ ID NO: 265:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1638 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

	GGCACGAGGC GCGGCAGCG GTGGCGGCGG CGCCCCCGG CGGGAGCCGT NCCCTTTCCC	60
5	GTGCGGGAGC GCGGGGYCGG GGYCCAGGG ANCCCGGMC ACGGAGAGCG GGAAGAGGAT	120
	GGATTGCCCG GCCCTCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
	AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAGAAGT TCAGAAGCAA	240
10	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGTATCTC AGCAGTTTTG ACTTCAGAAC	300
	TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT	360
15	CAATCAAAAT AAGGGTAAAC CAGACTTGAA TACAACATTG CCAATTAGAC AAACAGCATC	420
	AATTTTCAAA CAACCGGTAA CCAAAGTCAC AAATCATCCT AGTAATAAAG TGAATCAGA	480
	CCCACAACGA ATGAATGAAC AGCCACGTCA GCTTTTCTGG GAGAAGAGGC TACAAGGACT	540
20	TAGTGCATCA GATGTAACAG AACAAATAT AAAAACCATG GAACTACCCA AAGGTCTTCA	600
	AGGAGTTGGT CCAGGTAGCA ATGATGAGAC CCTTTTATCT GCTGTTGCCA GTGCTTTGCA	660
25	CACAAGCTCT GCGCCAATCA CAGGGCAAGT CTCCGCTGCT GTGGAAAAGA ACCCTGCTGT	720
	TTGGCTTAAC ACATCTCAAC CCTCTGCAA AGCTTTTATT GTCACAGATG AAGACATCAG	780
	GAAACAGGAA GAGCGAGTAC AGCAAGTACG CAAGAAATTG GAAGAAGCAC TGATGGCAGA	840
30	CATCTTGTCG CGAGCTGCTG ATACAGAAGA GATGGATATT GAAATGGACA GTGGAGATGA	900
	AGCCTAAGAA TATGATCAGG TAACTTTGCA CCGACTTTCC CCAAGAGAAA ATTCCTAGAA	960
35	ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA	1020
	TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTGTAGATG TATTTTGTAT GTATATATCT	1080
	ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAAATA	1140
40	TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG	1200
	TAGCACTTAC GTAAACATT TGTTCCTCCC ACAGTTTTAA TAAGAACAGA TCAGGAATTC	1260
45	TAAATAAATT TCCAGTTAA AGATTATGT GACTTCACTG TATATAAACA TATTTTATA	1320
	CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCTCA CTGTAAAGAC AAATAAATGA	1380
	TTATATTAC AGACTGATTG GAATTCCTTC TGTGAAAAG CACACACAAT AAAGAACCCC	1440
50	TCGTTAGCCT TCCTCTGATT TACATTCAAC TCTGATCCCG GGGCCTTAGG TTTGACATGG	1500
	GAGGTGGGAG GAAGATAGCG CATATATTTG CAGTATGAAC TATTGCCTCT GGGACGTTGT	1560
55	GAGGAATTGT GCTTTCACCA GAATTTCTAA GGATTTCTGG CTTAAATATC ACCTAGCCTG	1620
	TGGTAATTTT TTTTCCT	1638

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

10 CGTGGCTACT GCCATGCAGG TACCGGGTCC GGAATTCCCA GGGTCGACCC ACGCGTCCGC 60
TCAGTTGGCA AGGTACCTGG GAAATACTGT TGATCTCAGC AGTTTGTACT TCAGAACTGG 120
15 AAAGATGATG CCTAGTAAAT TACAGAAGAA CAAACAGAGA CTGCGAAACG ATCCTCTCAA 180
TCAAAATAAG GGTAAACCAG ACTTGAATAC AACATTGCCA ATTAGACAAA CAGCATCAAT 240
TTTCAACAA CCGGTAACCA AAGTCACAAA TCATCCTAGT AATAAAGTGA AATCAGACCC 300
20 ACAACGAATG AATGAACAGC CACGTCAGCT TTTCTGGGAG AAGAGGCTAC AAGGACTTAG 360
TGCATCAGAT GTAACAGAAC AAATTATAAA AACCATGGAA CTACCCAAAG GTCCTCAAGG 420
25 AGTTGGTCCA GGTAGCAATG ATGAGACCTT TTTATCTGCT GTTGCCAGTG CTTTGCACAC 480
AAGCTCTGCG CCAATCACAG GGCAAGTCTC CGCTGCTGTG GAAAAGAACC CTGCTGTTTG 540
GCTTAACACA TCTCAACCCC TCTGCAAAGC TTTTATTGTC ACAGATGAAG ACATCAGGAA 600
30 ACAGGAAGAG CGAGTACAGC AAGTACGCAA GAAATTGGAA GAAGCACTGA TGGCAGACAT 660
CTGTGCGCA GCTGCTGATA CAGAAGAGAT GGATATTGAA ATGGACAGTG GAGATGAAGC 720
35 CTAAGAATAT GATCAGGTAA CTTTCGACCG ACTTCCCCA AGAGAAAATT CCTAGAAATT 780
GAACAAAAT GTTCCACTG GCTTTGCCT GTAAGAAAAA AAATGTACCC GAGCACATAG 840
AGCTTTTAA TAGCACTAAC CAATGCCTTT TTAGATGTAT TTTTGATGTA TATATCTATT 900
40 ATTCAAAAAA TCATGTTTAT TTTGAGTCTT AGGACTTAAA ATTAGTCTTT TGTAATATCA 960
AGCAGGACCC TAAGATGAAG CTGAGCTTTT GATGCCAGGT GCAATCTACT GGAAATGTAG 1020
45 CACTTACGTA AACATTGTG TTCCCCACA GTTTTAATAA GAACAGATCA GGAATTCTAA 1080
ATAAATTTCC CAGTTAAAGA TTATTGTGAC TTCACTGTAT ATAAACATAT TTTTATACTT 1140
TATTGAAAGG GGACACCTGT ACATTCTTCC ATCRTCAGTG TAAAGACAAA TAAATGATTA 1200
50 TATTACAGA CTGATTGGAA TTCTTTCTGT TGAAAAGCAC ACACAATAAA GAACCCCTCG 1260
TTAGCCTTCC TCTGATTAC ATTCAACTCT GATCCCGGGG CCTTAGGTTT GACATGGGAG 1320
55 GTGGGAGGAA GATAGCGCAT ATATTTGCAG TATGAACTAT TGCCTCTGGG ACGTTGTGAG 1380
GAATTGTGCT TTCACCAGAA TTTCTAAGGA TTTCTGGCTT AAATATCACC TAGCCTGTGG 1440
TAATTTTTTT TCCCT 1455
60

(2) INFORMATION FOR SEQ ID NO: 267:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

15	CGCCTGCAGT ACCGGTCCGG AATTCCTGGG TCGACCCACG CGTCGCTGAC CCAGGAGAAG	60
	CTGCCTGTCT ACATCAGCCT GGGCTGCAGC GCGCTGCCGC CGCGGGGCCG GCAGCTGAAC	120
	TATGTGCTCT TCAGGGCGGG CACCGTGTG CATTCACTTT TGTACCCCA GCATCTAGCA	180
20	GTGTTGGCAT GTAGTAGGCA CTCAAGAAAT GTGTGTTGAA TGAACGATGC CTGTGACAAG	240
	CAAGCGGACT TTATTCTTTC CTGACCCTTG CTCCTATGAC ACACCTCTC CTGACTGCCA	300
	CTGTCACTCC TTCAGAGCAG AACTCCTCTA GGAACCTGG ATGGGAAACA GCCATGGCCA	360
25	AGGACATCCT GGTGAAGCA GGGCTACACT TTGATGAACT GAACAAGCTG AGGGTGTGG	420
	ACCCAGAGGT TACCCAGCAG ACCATAGAGC TGAAGGAAGA GTGCAAAGAC TTTGTGGACA	480
30	AAATTGGCCA GTTTCAGAAA ATAGTTGGTG GTTTAATTGA GCTTGTGTGAT CAACTTGCAA	540
	AAGAAGCAGA AAATGAAAAG ATGAAGGCCA TCGGTGCTCG GAACTTGCTC AAATCTATAG	600
	CAAAGCAGAG AGAAGCTCAA CAGCAGCAAC TTCAAGCCCT AATAGCAGAA AAGAAAATGC	660
35	AGCTAGAAAG GTATCGGGTT GAATATGAAG CTTTGTGTAA AGTAGAAGCA GAACAAAATG	720
	AATTTATTGA CCAATTATT TTTCAGAAAT GAACTGAAAA TTTCGCTTTT ATAGTAGGAA	780
40	GGCAAAACAA AAAAAAGCCT CTCAAAACCA AAAAAACCTC TGTAGCATTG CAGCGGCTTG	840
	ACCAATGACC TATGTCACAA GAGGTGGCGT GTAAGGAATG CAGCCCCCTG AAGACAGCAC	900
	TACAAGTCTG GGGGAGCCAG TTTTAACATC AGTGACAGC TGCTGCTGGT GGCCCTGCAG	960
45	TGTACGTTCT CACCTCTTAT GCTTAGTTGG AACTAAGCAG TTTGTAAACT TTCATCCTTT	1020
	TTTTTGTAAG TTCAAAAGC TTTGGAAGGA GARGCAATAA ATTTTGTGTT TCNAAATGGC	1080
50	TTGATG	1086

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(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

5 GGCACGGGAG CAGCCGGGCT GGTCTGCTG CGAGCCGGCG GCCCGGAGTG GGGCGGCGGA 60
 GCAAACATGA ACGTTGGAGT TGCCACAGT GAAGTGAATC CAAATACCCG TGTCATGAAC 120
 AGCCGGGGTA TGTGGCTGAC ATATGCATG GGAAGTTGGCT TGCTTCATAT TGTCTTACTC 180
 10 AGCATTCCTT TCTTCAGTGT TCCTGTTGCT TGGACTTTAA CAAATATTAT ACATAATCTG 240
 GGGATGTACG TATTTTTCGA TGCAGTGAAA GGAACACCTT TCGAAACTCC TGACCAGGGT 300
 15 AAAAGCAAGG CTCCTAACTC ATTGGGAACA ACTGGACTAT GGAGTACAGT TTACATCTTC 360
 ACGGAAGTTT TTCACAATTT CTCCAATAAT TCTATATTTT CTGGCAAGTT TCTATACGAA 420
 GTATGATCCA ACTCACITCA TCCTAAACAC AGCTTCTCTC CTGAGTGTAC TAATTCCCAA 480
 20 AATGCCACAA CTACATGGTG TTCGGATCTT TGGAAATTAAT AAGTATGAA ATGTTTGTAA 540
 ACTGAAAAAA AATTTTACAG CTACTGAATT TCTTATAAGG AAGGAGTGGT TAGTAAACTG 600
 25 CACTGTTTCT CTGATAATGT GAAATGAGAA GTATTTACAT TGGAGGGCCA ATGGCTGGTC 660
 CTTCAAGTGC TGTTTTGAAG TGCAGATTTT CATTAATGA TGCCTCTGTT TAATACACCT 720
 GGTACATTTT TGAAGAGGGG CTTTATAAGC AGGCTGGGCA GGGCCAGCTT ATAAGTTAAA 780
 30 GGGCATCACA GTGAGGGTGT AGTAGATAAA TTCAAGGAAA TAAGAGATTT GTAAGAACT 840
 AGGACCAGCT TAACTTATAA TGAATGGGCA TTGTGTTAAG AAAAGAACAT TTCCAGTCAT 900
 35 TCAGCTGTGG TTATTTTAAAG CAGACTTACA TGTAAACCGG AATCCTCTCT ATACAAGTTT 960
 ATTAAAGATT ATTTTATTA CCGTAAAAAA AAAAAAAAAA AAA 1003

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(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ATCAGCATCT ACAAGTAGCA TATTTTGGAT GGTGTTGTG TGCTACTTCA AAGTAACTAG 60
 GAAAAAATAA TCCTCGCAAC ACAGGTACCT TGTATGTCA GAATTGGGGG TGTTAGGTTG 120
 55 CCAGTTGTAT CAGTGTGAT TCATTTTATT ACTTCCTACA GAGCAAACAT GAACGTTGGA 180
 GTTGCCACCA GTGAAGTGAA TCCAAATACC CGTGTATGA ACAGCCGGG TATGTGGCTG 240
 60 ACATATGCAT TGGGAGTTGG CTTGCTTCAT ATTGTCTTAC TCAGCATTC CTTCTTCAGT 300

5 GTTCCTGTTG CTGGAACCTT AACAAATATT ATACATAATC TGGGGATGTA CGTATTTTGT 360
 CATGCAGTGA AAGGAACACC TTTCGAAACT CCTGACCAGG GTAAAGCAAG GCTCCTAACT 420
 CATTGGGAAC AACTGGACTA TGGAGTACAG TTTACATCTT CACGGAAGTT TTTCACAATT 480
 TCTCCAATAA TTCTATATTT TCTGGCAAGT TTCTATACGA AGTATGATCC AACTCACTTC 540
 10 ATCCTAAACA CAGCTTCTCT CCTGAGTGTA CTAATTCCCA AAATGCCACA ACTACATGGT 600
 GTTCGGATCT TTGGAATTAA TAAGTATTGA AATGTTTGA AACTGAAAAA AAATTTTACA 660
 GCTACTGAAT TTCTTATAAG GAAGGAGTGG TTAGTAAACT GCACTGTTTC TSTGATAATG 720
 15 TGAAATGAGA AGTATTTACA TTGGAGGGCC AATGGCTGGT CCTTCAAGTG CTGTTTGA 780
 GTGCAGATTT CCATTAAATG ATGCCTCTGT TTAATACACC TGGTACATTT CTGAAGAGGG 840
 20 GCTTTATAAG CARGCTGGGC AGGCCAGCT TATAAGTTAA AGGCATCAC AGTGAGGGTG 900
 TAGTAGATAA ATTCAAGGAA ATAAGAGATT TGTAAGAAAC TAGGACCAGC TTAACCTATA 960
 ATGAATGGGC ATTGTGTTAA GAAAAGAACA TTTCAGTCA TTCAGCTGTG GTTATTTAAA 1020
 25 GCAGACTTAC ATGTAAACCG GAATCCTCTC TATACAAGTT TATTAAAGAT TATTTTATT 1080
 ACCRTACATA TTTCKCTTGT TTTATGTAAG YGGATGTATA TCCTCTTGT TTATACAAGC 1140
 30 CAGTTCCAC TTATGAGGGT ACTTTTTTGG TTTGCTGGG CTTAATATTG TGTATTGGTC 1200
 AATGAGGCCA TTTTACANT TATTAACGTT ACAG 1234

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(2) INFORMATION FOR SEQ ID NO: 270:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 574 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

NGAGGTGCGT TCTGAGCCGT CTGTCCTGCG CCAAGATGCT TCAAAGTATT ATTAAAAACA 60
 TATGGATCCC CATGAAGCCC TACTACACCA AAGTTTACCA GGAGATTTGG ATAGGAATGG 120
 50 GGCTGATGGG CTTCAATGTT TATAAAATCC GGGCTGCTGA TAAAAGAAGT AAGGCTTTGA 180
 AAGCTTCAGC GCCTGCTCCT GGTCACTACT AACCAGATT ACTTGGAGTA CATGTGAAAG 240
 55 AAAACGTCAG TCTGCCTGTA AATTTTACCA AGCCGTGTTA GATGGGGAGC GTGGAACGTC 300
 ACTGTACACT TGTATAAGTA CCGTTTACTT CATGGCATGA ATAAATGGAT CTGTGAGATG 360
 CACTGCTACC TGGTACTGCT TTCAGTGTGT TCCCCCTCAG CCCTCCGGCG TGTGAGGCAT 420
 60

ACTCTGAGTA GATAATTTGT CATGCAGCGC ATGCAATCAG AATCTCACTG AGCCACCCAT 480
CATTGTGAAA TAATTACCTC AGTTGTACAG GACTTGGTGA TCAGGATCCA GGCACCTCACT 540
5 TGTATTCTAC TGCTCAATAA ACGTTTATTA AACT 574

10 (2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1731 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

20 GCTGCAAGGT GCGCCTCGTG CCGCTGCAGA TCCAGCTCAC TACCCTGGGA AATCTTACAC 60
CTTCAAGCAC TGTGTTTTTC TGCTGTGATA TGCAGGAAAG GTTCAGACCA GCCATCAAGT 120
ATTTTGGGGA TATTATTAGC GTGGGACAGA GATTGTTGCA AGGGGCCCGG ATTTTAGGAA 180
25 TTCTGTATAT TGTAACAGAA CAATACCCTA AAGGTCTTGG GAGCACGGTT CAAGAAATTG 240
ATTTAACAGG TGTAAACTG GTACTTCCAA AGACCAAGTT TTCAATGGTA TTACCAGAAG 300
30 TAGAAGCGGC ATTAGCAGAG ATTCCCGGAG TCAGGAGTGT TGTATTATTT GGAGTAGAAA 360
CTCATGTGTG CATCCAACAA ACTGCCCTGG AGCTAGTTGG CCGAGGAGTC GAGGTTTACA 420
TTGTGTCTGA TGCCACCTCA TCAAGAAGCA TGATGGACAG GATGTTTGCC CTCGAGCGTC 480
35 TCGCTCRARC CNGGGATCAT AGTGACCACG AGTGNAGGCT GTTCTGCTTC AGCTGGTAGC 540
TGATAAGGAC CATCCAAAAT TCAAGGAAAT TCAGAACTTA ATTAAGGCCA GTGCTCCAGA 600
40 GTCGGGTCTG CTTTCCAAAG TATAGGACAT TTGAAGAACT GGTATGCTAC TCACTGGTGA 660
AGGACAGTCA GGTGAAGGAC TGTAAGCCCA CACAAGCTCT TCTTATCTCT ACTAGAATTA 720
AAATGTTAAG TCAAAAACGG CTCCTTTTTT GCGCCTCCTA GTGAACCTTA CCAGCTAGAC 780
45 CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT CCGGTGCTGC TTACCTTCCT 840
TTTTTGTTAA TGTGCTTTTA TTTATTAAAA AAAATTACAA TGAAGATGCC TGTMTTGTCT 900
50 CTACTGTGTA CTCTGATCGT ATCTTTCCAA AGTGCAGACT CTGTGAAGT TTTCTTAAAT 960
TGTTCACTTT AAAGAAAATG ACGTACCAAC AATGATTTGG CTTTTATATT ACTGTAAGAT 1020
GTTATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG ATTGAITGGA ATAAGATTAT 1080
55 TGCATATGAA TTTACCCACA GGA CTCTGAA TCATGTTACC CACTCCCCCT ACAATGTTGT 1140
CCACTTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT GTTGAATAAT TACATATCTT 1200
60 TCTKGACTAT ACTGATTTCT TATTTTGGTC ACTATTACTA AATCTCTGTT AATATTCTCT 1260

CTTTTAACTG AAAAGGGATG GGATAGAAGG GTTTGCAATG CCATATTATT GGTGGAGGGC 1320
TGTTTTAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT ACCAACATCT TGAATATATA 1380
5 TTCTAGTGTC CACAAGATTT AGCAAAAAGA TAAAGCTTGG GTGGAATATC ATTTTAAAT 1440
GTTTCATGTTG TGTTCTATAT TTTCTTCACC TACTCTCCAA ATATTGTAAT GCAAAAAGTC 1500
10 TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAATGTT TCTCTTCGAT AAATTTATTT 1560
TCATTAAATA CTTRTTAGAG GGTTTTGAAA TGTTTTTCAA ATATGTGAAA TGTGAACTG 1620
CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG ATTGAAATTA TTTTGNCTC 1680
15 CACAAGATGG CTCTATGAGT ATTCTTCAG GGATCTTAAT ATTTATTTAA G 1731

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(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

30

CTGCTTAGGA AGAGAAGGTC AGAGTTGCGG GGGGCAGAGG CATTCCTGCC GCTGGCCCAG 60
TCACTATGTA GTGGAGGGGC AGACACCCTC CCGCAAATTC TGAAGGTTT TTAGTCTCGA 120
35 CTAGGGCAGT AGCCCAGGAC TCCTAGTCGC CGGCTTCAGG TCACTGCCGG CTGAACGGAG 180
CTGCCGTCGC CATGTTTGGC TGCTTGGTGG CGGGGAGGCT GGTGCAAACA GCTGCACAGC 240
AAGTGCAGA GGATAAATTT GTTTTGGACT TACCTGATTA TGAAAGTATC AACCATGTTG 300
40 TGGTTTTTAT GCTGGGAACA ATCCCATTTT CTGAGGGAAT GGGAGGATCT GTCTACTTTT 360
CTTATCCTGA TTCAAATGGA ATGCCAGTAT GGMAACTCCT AGGATTTGTC ACGAATGGGA 420
45 AGCCAAGTGC CATCTTCAAA ATTTCAAGTC TTAAATCTGG AGAAGGAAGC CAACATCCTT 480
TTGGAGCCAT GAATATTGTC CGAACTCCAT CTGTTGCTCA GATTGGAATT TCAGTGGAAT 540
TATTAGACAG TATGGCTCAG CAGACTCCTG TAGGTAATGC TGCTGTATCC TCAGTTGACT 600
50 CATTCACTCA GTTCACACAA AAGATGTTGG ACAATTTCTA CAATTTTGCT TCATCATTTG 660
CTGTCTCTCA GGCCCAGATG ACACCAAGCC CATCTGAAAT GTTCATTCCG GCAAATGTGG 720
55 TTCTGCAAAT GGTATGAGGC ATNMTCTGTC TCCAATATTA AGGCTTTTTA TAACTGAATA 780
TCTATTTTGT CTATGAATAT ATTCTTTTTC TGACATTTAA ACATATCTTT TTATTGTGAA 840
CATCAGCACT GCATGCCATT AAAGTATGTA CTATAGAGAT CTGATGAGAA ACAGTTCTTA 900
60

CCCTAAATAT TTGTTATAT TGTCGCCATT ATGAATTTAT AAAGACAGGA AAATATAGTT 960
 GCCTATGTTT TAGGGACCAC TATTAAAGCT TATAAATATT TGTGTATTTT CATTTAGAAG 1020
 5 TACCATCTAT GAGAGTAGTT TATACTGCAC TGTGTACATG AATGGCTAAT GAATCTATTT 1080
 TCCAACTTTC CCGTGTTTTA TAGATATTTT TTTTCACTTT GAGTATCCTA GAGATGGGAG 1140
 GATGCCTAGG AAGAGTTTGT TGAGAAGTGG TACCATGGTG TAGCATGGGA GAGCATTTGGG 1200
 10 AATGCACTAG GTTTGAATTT GGCATAATGG TAGCTATGTG ACCCTGAGCA AATTTCTCTC 1260
 ATCTGCTCAT CTGANGAATG AGGAAATAGG AGTGAATTTG ATNTTTCCTA GGTCCTCTA 1320

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(2) INFORMATION FOR SEQ ID NO: 273:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CCCTGGAGAG GGGCTGCTGT GCCAGCTTGG GGAGGGTCTG GGATGGGGCT GCCCCTGATG 60
 30 GCCCTGATGT GGAGTACCTT GCCAGCATCT GCTGGGGTGA ACTTTATTTT AGCCCTTCCC 120
 TTGTTGYTCT TATGAAGAAC AGAGGAGGGG TGGGCAGGTC AGTGATGTCA GCAGTGAGTA 180
 TTTCCAGCAC AGCGGCTCTG GAAGAGGCAT GAGGCATTTT TTTGAGAAA TGRTCATTAT 240
 35 TCAGCCAGAA GGCATTCAAT AAGTAAGTCC TGAATTTGTG CCCAGCTCTG TGTATAGGC 300
 CCTTGCGGAG ACTCAGGAGG GGCARAGGAC GCTAGKTTKT AGWTAACACG GAACCTCARA 360
 40 GGWTATATGG TCCAAGAAGA CCCGGGGGCG GTGAAAACCC TGTGGACTAA TGCTCACGGG 420
 AGCCCGAGGT CACACTTTGA CTTTGCTACC ATGGGCTGTG TCTANGNACG TATATATGCT 480
 GCGTAATTAT TACAGAGGCA GTCCATGTGC ATTGT 515

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(2) INFORMATION FOR SEQ ID NO: 274:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

TGACACCCAT AAGGAATTCA TGAAGAAAGT AGAAGAAAAG CGAGTGGACG TTAACCTCAGC 60

	AGTAGCCATG GGAGAAGTCA TCCTGGCTGT CTGCCACCCC GATTGCATCA CAACCATCAA	120
	ACACTGGATC ACCATCATCC GAGCTCGCTT CGAGGAGGTC CTGACATGGG CTAAGCAGCA	180
5	CCAGCAGCGT CTTGAAACGG CCTTGTGAGA ACTGGTGGCT AATGCTGAGC TCCTGGAAGA	240
	ACTTCTGGCA TGGATCCAGT GGGCTGAGAC CACCCTCATT CAGCGGGATC AGGAGCCAAT	300
10	CCCGCAGAAC ATTGACCGAG TTAAAGCCCT TATCGCTGAG CATCAGACAT TTATGGAGGA	360
	GATGACTCGC AAACAGCCTG ACGTGGACCG GGTACCAAG ACATACAAA GGAAAAACAT	420
	AGAGCCTACT CACGCGCCTT TCATAGAGAA ATCCCGCAGC GGAGGCAGGA AATCCCTAAG	480
15	TCAGCCAACC CCTCTCCCA TGCCAATCCT TTCACAGTCT GAAGCAAAA ACCCACGGAT	540
	CAACCAGCTT TCTGCCCCT GGCAGCAGGT GTGGCTGTTA GCACTGGAGC GGCAAAGGAA	600
20	ACTGAATGAT GCCTTGGATC GGCTGGAGGA GTTGAAAGAA TTTGCCAACT TTGACTTTGA	660
	TGTCTGGAGG AAAAAGTATA TCGTGTGGAT GAATCACAAA AAGTCTCGAG TGATGGATTT	720
	CTTCCGGCGC ATTGATAAGG ACCAGGATGG GAAGATAACA CGTCAGGAGT TTATCGATGG	780
25	CATTTTAGCA TCCAAGTCC CCACCACCAA GTTAGAGATG ACTGCTGTGG CTGACATTTT	840
	CGACCGAGAT GGGGATGGTT ACATTGATTA TTATGAATTT GTGGCTGCTC TTCATCCCAA	900
30	CAAGGATCGC TATCGACCAA CAACCGATGC AGATAAAATC GAAGATGAGG TTACAAGACA	960
	AGTGGCTCAG TGCAAATGIG CAAAAAGGTT TCAGGTGGAG CAGATCGGAG AGAATAAATA	1020
	CCGGTTCTTC CTCGGCAATC AGTTTGGGGA TTCTCAGCAG TTGCGGCTGG TCCGTATTCT	1080
35	GCGCAACCGT GATGGTTCGC GTTGGTGGAG GATGGATGGC CTGGGATGAA TTTTITAGTGA	1140
	AAAATGATCC CTGCCGAGCA CGAGGTAGAA CTAACATTGA ACTTAGAGAG AAATTCATCC	1200
40	TACCAGAGGG AGCATCCAG GGAATGACCC CCTTCCGCTC ACGGGGTCGA AGGTCCAAAC	1260
	CATCTTCCCG GGCAGCTTCC CCTACTCGTT CCAGCTCCAG TGCTAGTCAG AGTAACCACA	1320
	GCTGTACATC CATGCCATCT TCTCCAGCCA CCCCAGCCAG TGAACCAAG GTTATCCCAT	1380
45	CATCAGGTAG CAAGTTGAAA CGACCAACAC CAACTTTTCA TTCTAGTCGG ACATCCCTTG	1440
	CTGGTGATAC CAGCAATTAG TTCTTCCCCG GCCTCCACAG GTGCCAAAAC TAATCGGGCA	1500
50	GACCCTAAAA AGTCTGCCAG TCGCCCTGGG AGTCGGGCTG GGAGTCGAGC CGGGAGTCGA	1560
	GCCAGCAGCC GCGGAGGAAG TGACGCTTCT GACTTTGACC TCTTAGAGAC GCATTGCTTG	1620
	TTCCGACACT TCAGAAAGCA GCGCTGCAGG GGGCCAAGGC AACTCCAGGA GAGGGCTAAA	1680
55	CAAACCTTCC AAAATCCCAA CCATGTCTAA GAAGACCACC ACTGCCTCCC CCAGGACTCC	1740
	AGGTCCCAAG CGATAACACT GTCTAAGCAC CCCCAAGCCA CTATCCACTT TGAATCCTGC	1800
60	TCCATACATT GGGTGTATAT TTATTCTGAA CGGGAGAAGT TATATTGTTA AAAGTGTAAG	1860

AGAATAATG TGTATGAAG CTGCCTTATT TTTTTCCTT TTGTAAGTTA CTATTTTCAT 1920
 GTGAATATTT ATGTAGATAA AATTTGCCTC CTGGTAACCC TGTAATGGAT GGGGCCCAGA 1980
 5 AATGAAATAT TTGAGAAAA CAAGTGAAAA GGTCAAGATA CAAATGTGTA TTAACAAAAA 2040
 AAAAGCCTAT TAATAGGGTT TCTGCGCGGT GCAGGGTGT AAACCTGCTT TATCTTTTAG 2100
 GATTATTCCT AAATGCATCT TCTTTATAAA CTGACTTGC TATCTCAGCA AGATAAATTA 2160
 10 TATTAAAAA ATAAGAATCC TGCAGTGTCT AAGGAACCTT TTTTGTGTA ATCACGGACA 2220
 CCTCAATTAG CAAGAACTGA GGGGAGGGCT TTTCCATTG TTTAATGTTT TGTGATTTT 2280
 15 AGCTAAAGAG AGGGAACCTC ATCTAAGTAA CATTTGCACA TGGATACAGC AAAAGGAGTT 2340
 CATTCGAATA CTGTCTTTGG ATATTGTTTC AGTACTGGT GTTTAAAGGA CAAATAGCTG 2400
 CTAGAATTCA GGGGTAAATG TAAGTGTTC GAAAACGTC GAACATTTGG GGTMTTAAAC 2460
 20 TGATTTGTTG CTCCCTATCC AGCCTAGACA CCAGTAACTC TTGTGTTTAC CAGGACCCAG 2520
 ACCCTTGGCA AGGGATAGGC TCGTTGGTGA CATTTGTAAT TTCAGATTTG TTTTATCCAC 2580
 25 TTTTGTGCT ATTTATTTAA ATGGTCGATC AACTTCCCAC AACTGAGGA ATGAATTCCA 2640
 CGAGCCTGTT CTGAAATGT GGACGTAAGA CAAACACGTG CTCGTCTTT AATGGAGTTC 2700
 ACCAGCACAC TTGTTAACCA GTCCTGTTTG CTTCGCTCT TTTTGTGCG TAATAAAGTC 2760
 30 AACTGACCAA GTGACCATGA AAAGGGGCTG TCTGGGCTC CTGTTTMTTA GCTGCTGTTT 2820
 TTCAGCTCCG ACCATGTTGC TGTGTGATTA TCTCAATTGG TTTTAATTGA GGCAGAACT 2880
 35 GAAGCTCTAC CAATGAACTG TTTAGAAACA AGACACACTT TTGTATTAAA ATTGCTTGCA 2940
 GTAACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAACTCG AGGGGGGCCC GGTAC 2995

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(2) INFORMATION FOR SEQ ID NO: 275:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1990 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

GGGACCCGCG CGSCTCCCGG GGATGGTGAG CAAGGCCTG CTGCNWCCTG TCTGCCGTCA 60
 ACCGCAGAGG ATGAAGCTGC TGCTGGGCAT CGCCTTGCTG GCCTACGTCG CCTCTGTTTG 120
 55 GGGCAACTTC GTTAATATGA GGTCTATCCA GGAAATGGT GAACTAAAAA TTGAAAGCAA 180
 GATTGAAGAG ATGGTTGAAC CACTAAGAGA GAAATCAGA GATTTAGAAA AAAGCTTTAC 240
 60 CCAGAAATAC CCACCAGTAA AGTTTTTATC AGAAAAGGAT CGGAAAAGAA TTTTGAWTAA 300

	CAGGAGGCGC AGKGTTCGTG GGCTCCCATC TKAACGACA AACTCATGAT GGACGGCCAC	360
	GAGGTGACCG TGGTGGACAA TTTCTTCACG GGCAGGAAGA GAAACGTGGA GCACTGGATC	420
5	GGACATGAGA ACTTCGAGTT GATTAAACCAC GACGTGTGGG AGCCCCCTCTA CATCGAGGTT	480
	GACCAGATAT ACCATCTGGC ATCTCCAGCC TCCCTCCAA ACTACATGTA TAATCCTATC	540
10	AAGACATTAA AGACCAATAC GATTGGGACA TTAAACATGT TGGGGCTGGC AAAACGAGTC	600
	GGTGGCCGTC TGCTCCTGGC CTCCACATCG GAGGTGTATG GAGATCCTGA AGTCCACCCT	660
	CAAAGTGAGG ATTACTGGGG CCACGTGAAT CCAATAGGAC CTCGGGCCTG CTACGATGAA	720
15	GGCAAACGTG TTGCAGAGAC CATGTGCTAT GCCTACATGA AGCAGGAAGG CGTGGAAAGTG	780
	CGAGTGGCCA GAATCTTCAA CACCTTTGGG CCACGCATGC ACATGAACGA TGGGCGAGTA	840
20	GTCAGCAACT TCATCCTGCA GGCCTCCAG GGGGAGCCAC TCACGGTATA CGGATCCGGG	900
	TCTCAGACAA GGGCGTTCCA GTACGTCAGC GATCTAGTGA ATGGCCTCGT GGCTCTCATG	960
	AACAGCAACG TCAGCAGCCC GGTCAACCTG GGAACCCAG AAGAACACAC AATCCTAGAA	1020
25	TTTGCTCAGT TAATTAAAAA CCTTGTGGT AGCGGAAGTG AAATTCAGTT TCTCTCCGAA	1080
	GCCCAGGATG ACCCACAGAA AAGAAAACCA GACATCAAAA AAGCAAAGCT GATGCTGGGG	1140
30	TGGGAGCCCG TGGTCCCGCT GGAGGAAGGT TTAAACAAAG CAATTCACTA CTTCCTGAAA	1200
	GAACTCGAGT ACCAGGCAAA TAATCAGTAC ATCCCCAAC CAAAGCCTGC CAGAATAAAG	1260
	AAAGGACGGA CTCGCCACAG CTGAACTCCT CACTTTTAGG ACACAAGACT ACCATTGTAC	1320
35	ACTTGATGGG ATGTATTTTT GGCTTTTTTT TGTGTGCTT TAAAGAAAGA CTTTAACAGG	1380
	TGTCATGAAG AACAACTGG AATTTCAATC TGAAGCTTGC TTTAATGAAA TGGATGTGCC	1440
40	TAAAAGCTCC CCTCAAAAAA CTGCAGATTT TGCCTTGCAC TTTTGAATC TCTCTTTTAA	1500
	TGTAAAATAG CGTAGATGCA TCTCTGCGTA TTTTCAAGTT TTTTATCTT GCTGTGAGAG	1560
	CATATGTTGT GACTGTGCTT GACAGTTTTA TTTACTGGTT TCTTTGTGAA GCTGAAAAGG	1620
45	AACATTAAGC GGGACAAAAA ATGCCGATTT TATTTATAAA AGTGGGTACT TAATAAATGA	1680
	GTCGTTATAC TATGCATAAA GAAAAAYCCT AGCAGTATTG TCAGGTGGTG GTGCGCCGGC	1740
50	ATTGATTTTA GGCAGATAA AAGAATCTG TGTGAGAGCT TTATGTTTCT CTTTAAATTC	1800
	AGAGTTTTTC CAAGGTCTAC TTTTGAGTTG CAAACTTGAC TTTGAAATAT TCCTGTTGGT	1860
	CATGATCAAG GATATTTGAA ATCACTACTG TGTTTTGCTG CGTATCTGGG GCGGGGGCAG	1920
55	GTTGGGGGGC ACAAAGTTAA CATATTCCTG GTTAACCATG GTTAAATATG CTATTTTAAT	1980
	AAAATATTGA	1990
60		

(2) INFORMATION FOR SEQ ID NO: 276:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

AACTTCGCTT AGCTCTCCAG GGTNAAACGG GTGAGNCCTT AAAACAGAA GAGAACAAGA 60
15 TTAAAGTCC GTTGCAATTGA AAATAACAAA CAATATCAAT GTTTTAATCA AGGATCTCTT 120
CCACATTCCT CCTTCTTATA AGAGCACAGT AACACTATCC TGGAAACCTG TACAAAAGGT 180
TGAGATTGGG CAAAAGAGAG CCACTGAAGA TACAACCTCA GGTTCCACCAC CCAAGAAATC 240
20 TTCAGCAGGA CAAAAAGAG ATGCCAGGCA GATTTATAAC CCTCCCAGTG GGAAATATAG 300
CAGCAATTTG GGCAACTTTA ATTATGAGCA GAGAGGAGCC TTCAGGGGAA GTAGAGGTGG 360
25 CCGAGGTTGG GGCACACGAG GAAATCGTAG TCGGGGAAGA CTCTACTGAA TAAGACATCA 420
GCATTCTTCA GCATTGTCAT GAGCTTAATA TACTTAAATT CTACTACTCA TTGGATTGCC 480
GGGGATGTCC CTTTAAACAG ACTGCTGCCT TCAGCTAAAA ACTTAATGTT CTTTATACCT 540
30 TTGTATGTAT GACCTACTTT TGTAACAGAC CATGGTTGTG TCCAAGGTAA AACCACAGTG 600
ATATTTTTGG ATGCTTTGTC TGCAATCTTG ACTTGTTTTT GCAGTATCAT TATTCAGACT 660
35 TCAAATGTG AATCTTTTAA ACATCTTGAT AATTGTGTG TGAGAGCTGT TCATTCTAAA 720
ATGTAATGAA ATTCAGTCTA GTTCTGCTGA TAAAGATCAT CAGTTTTGAA AGGTTACTGA 780
TTTTCTCTTT CCTCTTAGT TTTTACCCA ATATATGGAG AAGAGTAATG GTCAATCTTA 840
40 ACAATTTGTT TTAATTGTTT AATAAGCTG CTGGGCAGTG GTGCAGCATT CCTACCTAGT 900
GTCATAAAG CAAAATACTT ACATAGCTTT CTAAATATAT AGGAATGACA TTACATTTTT 960
45 AGGAGAAAGT AAGTTGCTTT GCACCGCTA CTTAATCTTT TTCCATATAT TGTGATACAA 1020
ACTTTTGAAT ATGGAATCTT ACTATTTGAA TAGAAATGTG TATGTATAAT ATACATACAT 1080
ACATAAGCAT ATATGTGTGT GTGTGTGTGT ATATATATAT ATATGCATGC TGTGAAACTT 1140
50 GACTACACAA CATAAATCAC TTTTAAATTT CCAGGAACGG GTAGTCTGAC ACGGTGATTA 1200
TCCTTTTGAG GCTGAATCCG TTATTAACCT GTTATTTAGG TTTTACTCC CAGTAGCAAG 1260
55 GGATTCTAAG TTAGTTGCAC TTACATGATT ATTGTTATTT AAAACTAAGA ATAAAGGCTG 1320
CATTTTCAAA GATAAATTGG AATTGCTGTT GGTGAAATAA CAACCAAAAT ACTGAATCTG 1380
ATGTACATAC AGGTTTCTAC AGGAAGAGAT GGTATAATTT ACAATTTGGA GATTTAATAA 1440
60

	CCAGGGCTAC CCAGAAAAAG TGACTTGATA ACATGGTACC AATAAGTAAG GGATGCTCTC	1500
	TCGGTTTGCT TTTGCCACTT TCAAGATTTT AACTTCTCAG GTTATTATC AAAATTATTG	1560
5	TATAAGTTAG CCAATAGAAT TTTTAGGTTA AAACAACAGA TGGGGGGTTT GTGGAGTGT	1620
	TAATGTCATG GGCATTTTTA GTAGCATAGA CCCTTTGTTT TGCATTTGAA TGTTCGTAT	1680
	ATTTTGTGTT CACAGTTAAT CTTCCCTCCC CAAGTTTGCT ATTCAAATCA ACTGCCTGAA	1740
10	TGACATTTCT AGTAGTCTGA TGTATTTTTC TGAGGAATAG TTTGTGATTC CAATGCAGGT	1800
	GTCTTCATTA CCATTACCTC TACACTGCAG AAGAAGCAAA ACTCCTTTAT TAGAATTACT	1860
15	GCACATGTGT ATGGGGAAAA TAGTTCTGAA AGGCTAGAAT GATACAAGTG AGCAAAAGTT	1920
	GGTCAGCTTG GCTATGGAGT GGTGGCAATA ATCTCTAAAC ATTCCAAAAG ACCATGAGCT	1980
	GAACCTAAAC TCCCTTGGA TCTGAACAAA GGAATATAAA ATTGCCATTT GAAAACCTGAC	2040
20	CAGCTAATCT GGACCTCAGA GATAGATCAG CCAGTGGCCC AAAGCCATTT CAAGTACAGA	2100
	AATTATAGAG ACTACAGCTA AATAAATTTG AACATTAAAT ATAATTTTAC CACTTTTGT	2160
25	CTTTATAAGC ATATTTGTAA ACTCAGAAGT GAGCAGAAGT GACTTTACTT TCTCAAGTTT	2220
	GATACTGAGT TGACTGTTC CTTATCCCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA	2280
	GTGCACAACT TAGGTATTTT TTGCTTCCGA ATTTGAATGA AAAACTTAAT GCCATGGATT	2340
30	TTTTTCTTTT GCAAGACACC TGTATTATCAT CTTGTTTAAA TGTAAATGTC CCCTTATGCT	2400
	TTTGAAATAA ATTTCCCTTT GTAATTTTAA AAAAAA	2436
35		

(2) INFORMATION FOR SEQ ID NO: 277:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

	GCCACTGACT TCTCCACCC TTCTGTCTCC CCCATAATAG TTTATTTGGT TGGTCTGGAC	60
50	TCACTGTGTT CCTTTRATTA AATTCCTAAG GGCCTGAAG AAGACATTTT TACTGCAGAG	120
	GGTTAGAGGC ACTTGAGCAA GGCCCCACA TCCCAACTCT GGGAGTTGTG GTGGGAGGAG	180
	GCACCTCTGG GGGATAGGAC CAGACAAGAT AACAGGAGCT CACATGGNAA GCAGAAGCTG	240
55	TGACAAGTTT AGTAGTCCCA AAATGGGTTA TATCCCTTCC CCCTTTACAT CAGAATCTTG	300
	TGAAATGGGA AAACAACAGA AGGAGGGGAT CAAAGATAGC TGATCTCACA TGCTTCCCAG	360
60	GCAGGGCARG GGTGGGAGTC AAACCCGGGT GACAGGTGGG TGGAGAGCCC TGTTTGAGGT	420

5 TGTGGCTGAT CCTCTCTGG TATTAGTTTT TCCCCTGGGA GCAGGAAGCC CTAGGAAGAG 480
GGGACTGCAG GGTCCCCRGG GGATCTTTCC TCCCTCCCCT GCATGAGGCA GAGGCAAGCT 540
GCCTGCCAAC CCCCTCCCTC AAGGAATGGC CTGCCCAGG AATGCCACC ACACATACCC 660
TCTTCTTTTT TTCTAGTCAA ACTCTTGTTF ATTCCTTGGC TTGCCTCCCT CCTTCTCTCC 720
10 CTCTCAACCT TTA CTCTCTGA TTTCTATTTT ATGGAATTTG GGATTGAAGT TAAACTACAA 780
CAGTGCCGCC AACACCAAGT CTGTCAGGAA AAAAATACAA AGAAATTTAA CAAAAAAAAA 782
15 AA

20 (2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 961 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

30 GAGTTCCGGC TGGAGACCCG TGCTCTGGGC CGGCGCCTTC ACCATGGCCT CGGCAGAGCT 60
GGACTACACC ATCGAGATCC CGGATCAGCC CTGCTGGAGC CAGAAGAACA GCCCCAGCCC 120
AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC TGTGGTGATT CTYTTGGGCT GGGGTGGCTG 180
35 CAAGGACAAG AACCTTGCCA AGTACAGTGC CATCTACCAC AAAAGGGGCT GCATCGTAAT 240
CCGATACACA GCCCCGTGGC ACATGGTCTT CTCTCTCGAG TCACTGGGTA TCCCTTCACT 300
TCGTGTTTTG GCCCAGAAGC TGCTCGAGCT GCTCTTTGAT TATGAGATTG AGAAGGAGCC 360
40 CCTGCTCTTC CATGTCTTCA GCAACGGTGG CGTCATGCTG TACCGCTACG TGCTGGAGCT 420
CCTGCAGACC CGTCGCTTCT GCCGCCTGCG TGTGGTGGGC ACCATCTTTG ACAGCGCTCC 480
45 TGGTGACAGC AACCTGGTAG GGGCTCTGCG GGCCCTGGCA GCCATCCTGG AGCGCCGGGC 540
CGCCATGCTG CGCCTGTTGC TGCTGGTGGC CTMTGCCCTG GTGGTCGTCC TGTTCACGT 600
CCTGCTTGCT CCCATCACAG CCTCTTTCCA CACCCACTTC TATGACAGGC TACAGGACGC 660
50 GGGCTCTGCG TGGCCCCGAGC TCTACCTCTA YTCGAGGGCT GACGAAGTAG TCCTGGCCAG 720
AGACATAGAA CGCATGGTGG AGGCACGCCT GGCACGCCGG GTCCTGGCGC GTTCTGTGGA 780
55 TTTCGTGTCA TCTGCACACG TCAGCCACCT CCGTGA CTACTTACT ACACAAGCCT 840
CTGTGTCGAC TTCATGCGCA ACTGCGTCCG CTGCTGAGGC CATGCTCCA TCTCAMCTCT 900
GCTCCAGAAA TAAATGCCTG ACAMCTCCCC AAAAAAAAAA AAAAAAAAAA ACTCGAGGGG 960
60

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961

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(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

15

CGCGCTTTGC AGTTCGGTCT CCTGGGTAC GGCCAACGCC AAGTAGGGGA TTGCGTTCCC 60

TCCAGTCGCA GCCCTATCAG ATTTGGATAT GTCCTTCATA TTTGATTGGA TTTACAGTGG 120

20

TTTCAGCAGT GTGCTACAGT TTTTAGGATT ATATAAGAAA ACTGGTAAAC TGGTATTTCT 180

TGGATTGGAT AATGCAGGAA AAACAACATT GCTACACATG CTAAAAGATG ACAGACTTGG 240

ACAACATGTC CCAACATTAC ATCCCACCTTC CGAAGAACTG ACCATTGCTG GCATGACGTT 300

25

TACAACCTTTT GATCTGGGTG GACATGTTCA AGCTCGAAGA GTGTGGAAAA ACTACCTTCC 360

TGCTATCAAT GGCATTGTAT TTCTGGTGGG TTGTGCAGAC CACGAAAGGC TGTTAGAGTC 420

30

AAAAGAAGAA CTGTATTCAC TAATGACAGA TGAAACCATT GCTAATGTGC CTATACTGAT 480

TCTTGGGAAT AAGATCGACA GACCTGAAGC CATCAGTGAA GAGAGGTTGC GAGAGATGTT 540

TGGTTTATAT GGTCAGACAA CAGGAAAGGG GAGTATATCT CTGAAAGAAC TGAATGCCCG 600

35

ACCCCTTAGAA GTTTTCATGT GTAGTGTGCT CAAAAGACAA GGTTACGGAG AAGGCTTCCG 660

CTGGATGGCA CAGTACATG ATTAACACAA ACTCACATTG GTTCCAGGTC TCAACGTTCA 720

40

GGCTTACTCA GAGATTTGAT TGCTCAACAT GCATAACTTG AATTCAATAG ACTTTTGCTG 780

GTTATAAAAC AGATGTTTTT TAGATTATTA ATATTAAATC AACTTAATTT GAATGAGAAT 840

TGAAAACCTGA TTCAAGTAAG TTTGAGTATC ACAATGTTAG CTTTCTAATT CCATAAAAGT 900

45

ACTTGGTTTT TACAGTTTAT AATCTGACAT CACCCAGCG CCATTTGTAA AGAGCAACTT 960

TCCAGCAGTA CATTTGAAGC ACTTTTAAAC AACATGAAAC TATAAACCAT ATTTAAAAGC 1020

50

TCATCATGTT AAATTTTTTA TGTACTTTTC TGGAAGTAGT TTTTAAATTT TAGATTATAT 1080

GTCCACCTAT CKTAAGTGTA CAGTTAATAA TTAGCTTATT CAATGATGTC ATGATGCCTT 1140

ACAGTTTCA ATAACCTTTT TTCTTATGCA AACGTCATGC AATAAAACAA ACTCTAATGT 1200

55

TTGGCAAAAA AAAAAAAAAA AAANTCGA 1228

60

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

10 TCTCGGTCT CCGGACAGGT GAGCACCCTG ATGAAGGCCA CGGTCTGAT GCGGCACCTG 60
GCGGGTGCA GGAGATCGTG GCGCCCTCC GCAAGGCGS CGGAGACCGG TTACAGGTGA 120
15 TTTCTGATTT TRACATGACC TTGAGCAGGT TTGCATATAA TGGAAGCGA TGCCCTTCTT 180
CTTACAATAT TCTGGATAAT AGCAAGATCA TCAGTGAGGA GTGTGCGAAA GAGCTCACAG 240
CGCTCCTTCA CCACTATTAC CCAATTGAGA TCGACCCACA CCGGACCGTC AAGGAGAAGC 300
20 TACCTCATAT GGTGGAATGG TGGACCAAAG CGCACAATCT CCTATGTCAG CAGAAGATTC 360
AGAAGTTTCA GATAGCCCAG GTGGTTAGAG AGTCCAATGC AATGCTCAGG GAGGGATATA 420
25 AGACCTTCTT CAACACACTC TACCATAACA ACATTCCCCT TTTCATCTTT TCTGCGGGCA 480
TTGGTGATAT CCTGGAAGAA ATTATCCGAC AGATGAAAGT GTTCCACCCC AACATCCACA 540
TCGTGTCTAA CTACATGGAT TTTAATGAAG ATGGTTTCTT CCAGGGATTT AAGGGCCAGC 600
30 TGATACACAC ATACAACAAG AACAGCTCTG TGTGTGAGAA CTGTGGTTAC TTCCAGCAAC 660
TTGAGGGCAA AACCAATGTC ATCCTGCTGG GAGACTCTAT CCGGGACCTC ACCATGGCCG 720
35 ATGGGGTTCC TGGTGTGAG AACATCTCTA AAATTGGCTT CCTGAATGAC AAGGTGGAGG 780
AGCGGCGGGA NCGCTAACAT GGAATCCTAT GACATCGTGC TGGAGAAGGA CGAGACTCTG 840
GATGTGGTCA ACGGGCTACT GCAGCACATC CTGTGCCNAG GGGGTCCAGC TGGAGATGCA 900
40 AGGCCCCCTGA AGGCGCAGGC TCCNAAGKCC SCTGCAGGCC GTGGTGAGGA GGGGCGCCTC 960
CCCAGAGTCT GCTCCCCCGT GAACACAGAG CAGAGCCAGG GTGGCCAGCA GTGGCTGGGT 1020
45 CCTTCGCGC CCCTCCGTCC TCCTTTCCCT GAGCACCTTC ATCACCAGAG GCTTGAAGGA 1080
ACCCCGCCAT GTGGCAGGC ACAGGCACTG TTCCTGGTGA ACCTTGACC ACAGCATGTC 1140
AGTGCTCTAG GGATGTCTA CTCCAGGAT TTTCTTCAAA ATTTTAAAC ATGGAAGTT 1200
50 CAAACAAATA TAATGTGTGA AACAGATCAA AATTTTAAA ATGAAAAAA AGCTGCTCTG 1260
ATTGAGGGA TGTGGTCCG GGTAGAACCT GGACCTCTG GCCTGGGGC ACATGGGATG 1320
55 CTCTAG 1327

60 (2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

10 TCACCCTGCC TACAGCGTGG AGCTCAGATG ACTGCGCCCT CCACGGTCAC TGTGAGCAGG 60
TGGTATTCAC AGCCTGCATG ACCCTCACGG CCAGCCCTGG GGTGTTCCCC GTCAGTGTGT 120
GGCTTTGGCT GAAGCCTAAT TCCACAGCTC CTTGTTTTTT GAGAGAGACT GAGAGAACCA 180
15 TAATCCTTGC CTGCTGAACC CAGCCTGGGC CTGGATGCTC TGTGAATACA TTATCTTGCG 240
ATGTTGGGTT ATTCCAGCCA AAGACATTTT AAGTGCCTGT AACTGATTGT TACATATTTA 300
20 TAAAAATCTA TTCAGAAATT GGTCCAATAA TGCACGTGCT TTGCCCTGGG TACAGCCAGA 360
GCCCTTCAAC CCCACCTTGG ACTTGAGGAC CTACCTGATG GGACGTTTCC ACGTGTCTCT 420
AGAGAAGGAT TCCTGGATCT AGCTGGTCAC GACGATGTTT TCACCAAGGT CACAGGAGCA 480
25 TTGCGTCGCT GATGGGGTGT AAGTTTGTTT TGGTCTTGT TTCAGCCCAA TATGTAGAGA 540
ACATTGAAA CAGTCTGCAC CTTTGATACG GTATTGCATT TCCAAAGCCA CCAATCCATT 600
30 TTGTGGATTT TATGTGTCTG TGGCTTAATA ATCATAGTAA CAACAATAAT ACCTTTTTCT 660
CCATTTTGCT TGCAGGAAAC ATACCTTAAG TTTTTTTTGT TTTGTTTTTG TTTTTTGT 720
TTTTGTTTTT CTTTATGAAG AAAAAATAAA ATAGTCACAT TTTTAATACY AAAAAATGGA 780
35 CAAAAAAGT CGAGGGGGG 799

40

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 2196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

50 AAAGACTCTA ACATCCATGA GCTTGAACAT GAGCAAGAGC CTAATTGTGC CKSCCAGATG 60
GCTGAGCCCT TCCGTACCTT CCGAGATGGA TGGGTCTCCT ACTACAACCA GCCTGTGTTT 120
55 CTGGCTGGCA TGGGTCTTGC TTTCTTTTAT ATGACTGTCC TGGGCTTTGA CTGCATCACC 180
ACAGGGTACG CCTACACTCA GGGACTGAGT GGTTCATCC TCAGTATTTT GATGGGAGCA 240
TCAGCTATAA CTGGAATAAT GGGAACTGTA GCTTTTACTT GGCTACGTGC AAAATGTGGT 300
60

	TTGGTTCGGA CAGGTCTGAT CTCAGGATTG GCACAGCTTT CCTGTTTGAT CTTGTGTGTG	360
	ATCTCTGTAT TCATGCCTGG AAGCCCCCTG GACTTGTCCG TTTCTCCTTT TGAAGATATC	420
5	CGATCAAGGT TCATTCAAGG AGAGTCAATT ACACCTACCA AGATACCTGA AATTACAAC	480
	GAAATATACA TGTCTAATGG GTCTAATTCT GCTAATATTG TCCCGGAGAC AAGTCCTGAA	540
	TCTGTGCCCC TAATCTCTGT CAGTCTGCTG TTTGCAGGCG TCATTGCTGC TAGAATCGGT	600
10	CTTTGGTCTT TTGATTTAAC TGTGACACAG TTGCTGCAAG AAAATGTAAT TGAATCTGAA	660
	AGAGGCATTA TAAATGGTGT ACAGAACTCC ATGAACATATC TTCTTGATCT TCTGCATTTT	720
15	ATCATGGTCA TCCTGGCTCC AAATCCTGAA GCTTTTGGCT TGCTCGTATT GATTTTCAGTC	780
	TCCTTTGTGG CAATGGGCCA CATATATGTAT TTCCGATTTG CCCAAAATAC TCTGGGAAAC	840
	AAGCTCTTTG CTTGCGGTCC TGATGCAAAA GAAGTTAGGA AGGAAAATCA AGCAAATACA	900
20	TCTGTTGTTT GAGACAGTTT AACTGTTGCT ATCCTGTTAC TAGAATTATAT AGAGCACATG	960
	TGCTTATTTT GTACTGCAGA ATTCCAATAA ATGGCTGGGT GTTTTGCTCT GTTTTTACCA	1020
25	CAGCTGTGCC TTGAGAACTA AAAGCTGTTT AGGAAACCTA AGTCAGCAGA AATTAAC	1080
	TTAATTTCCC TTATGTTGAG GCATGGAAAA AAAATTGGAA AAGAAAAACT CAGTTTAAAT	1140
	ACGGAGACTA TAATGATAAC ACTGAATTCC CCTATTTCTC ATGAGTAGAT ACAATCTTAC	1200
30	GTAAAAGAGT GGTTAGTCAC GTGAATTCAG TTATCAATTG ACAGATTCCT ATCTGTACTA	1260
	GAATTCAGAT ATGTCAGTTT TCTGCAAAAC TCACTCTTGT TCAAGACTAG CTAATTTATT	1320
35	TTTTTGCATC TTAGTTATTT TTA AAAACAA ATTCCTCAAG TATGAAGACT AAATTTGAT	1380
	AACTAATATT ATCCTTATTG ATCCTATTGA TCTTAAGGTA TTTACATGTA TGTGGAAAA	1440
	CAAAACACTT AACTAGAATT CTCTAATAAG GTTTATGGTT TAGCTTAAAG AGCACCTTTG	1500
40	TATTTTATT ATCAGATGGG GCAACATATT GTATGAAGCA TATGTAGCAC TTCACAGCAT	1560
	GGTTATCATG TAAGCTGCAG GTAGAAGCAA AGCTGTAAAG TAGATTTATC ACACAATGAC	1620
45	TGCATACAGA CTTCAAATAT GTCAATAGTT TGGTCATAGA ACCTAGAAGC CAAAAGCCAC	1680
	ACAGAAGGGC AAGAATCCCA ATTTAACTCA TGTTATCATC ATTAGTGATC TGTGTTGTAG	1740
	AACATGAGGG TGTAAGCCTT CAGCCTGGCA AGTTACATGT AGAAAGCCCA CACTTGTGAA	1800
50	GGTTTGTGTT TACAAATCAC TTGATTTAAC AACTCAGGT AGAATATTTT TATTTTACT	1860
	GTTTTATACC CAGAAGTTAT TTCTACATTG TTCTACAGCA AGAATATTCA TAAAAGTATC	1920
55	CCTTTCAAAT GCCTTTGAGA AGAATAGAAG AAAAAAGTT TGTATATATT TAAAAAATT	1980
	GTTTTAAAAG TCAGTTTGCA ACATGCTCTG ACCAAGATGG TACTTTGCCT TAACCGTTTA	2040
60	TATGCACTTT CATGGAGACT GCAATACGTT GCTATGAGCA CTTTCTTTAT CCTTGGAGTT	2100

TAATCCTTTG CTTTCATCTTT CTACAGTATG ACATAATGAT TTGCTATGTT GTAAAAATCTT 2160
TGTAATAAAT TTCTATATAA AATATTGAA ACTTAA 2196

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(2) INFORMATION FOR SEQ ID NO: 283:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1185 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

GCAGTTAAGG CTTCTGATAA GGAAAGAGAG TCTGAACAGA GCACACACAT CTGGAGCTCC 60
20 AGGAGTGGGG GATGCAGCAT CAGATTCCAT CTTGAATTTT TGCTAAAATA CTTTGTACTC 120
ATAATGGATC TCAACAAAGA TCTGTATTTT ATCTGTGGCT CCATCTTCCC TCTGGGTCAA 180
GTAGATGTTA AGCTGGACCT TGGCAGCCTT CTTAACATGA AGAGATCTAG CTAGACAGAC 240
25 AGACTCCCCC ATTTATGGGA ACAAGAATTC AATTTATTCT CTATTATATA AACATTTTTT 300
TAAAGTGCCT TGGGTATAAA AATCTAAATG TCTGCGGTGT GATCAGTCAG GAGCACGTAA 360
30 CTATCACTCT TCGCATCCTT TGGTCACTGG GAGATCCTTT GGGGGCTGGG AGGTCCTTCT 420
GTCCCAGGCT AAAGGAAAAG CTTTACAAGG GTAAGAGCCA CAGAACCCTC GGCAAGAAAAG 480
GCCCGTCAGG GAGAATGAAT GGTACAGAGA GGAAAGGAAG GAAAGGGGGT GGAACAGAGG 540
35 TAGAAGGCAA GGAAGGGATG CCGCACTGGA GACCGATGGG GACACTCTAA TTGTGCAAGA 600
GGGAGGATCT TCCTTCTTGA ATGCTGAACA CAGCTAGTCT GAACCTTCCT TGGAAAGTCC 660
40 AGCTGTTTGC CCATGCATAG GGCCAACCTT CCCTGCAAAG CAGCAAATGT GGCTTCTATC 720
AGGAAGGAAA AGTATCCATC AGTGTGACAA GAGGTCACCT TCGAACTTGC ATGAACTCCT 780
TGCGCAGCCA CAAAGAGTCC TGGTAGAAGT GAGGATCGCC TAGTCTTACG GCTGTCCGTT 840
45 TATAGAAGTA GCAGTACAAC ACTGCTGCTA GTCTCTGGAA TACAAACAGC ATTTGAAGTC 900
CATCTGTCCA TATGAAGCTG TTGGAGTTTT TCCAGCGTAA GTTCATGACC CAGACATGAA 960
50 GGGAGATGCT GAGGGCAAAG TACACAGCTG TCAGGATGAT GGTCCCTTTG AACTTATGGA 1020
ATAGGAGGTT GACCAGGCCA GCCTGGAAGA CGAAGGTGTT GAAGAACATG AGGAAAATGA 1080
TGATGATGTT GAAGAGGACT GCAATATCCT GGATGCACTG AGGGAGAGGY TTCTAGTTCC 1140
55 TTTGAATGAG AGCTGTTTCC CTTGCTCTAA GGCAAGCACC TCCAA 1185

60

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1634 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

10

AGGGAAAGGG GAGGGTAGCG GGAGGGTAGC AGGTGAGTTC CTAGGGCTGG AAGGTTTAGC 60
AGCAGCCTGG TGCAGTGCCC TGTCAACAAG ACAAACCCAC GGTCTMCTG GGTGCCTACC 120
15 AAGCTTGGTT TGTACAAAAG CAAGGTGGGA GTCTATTTT GTACATGAGA TACATCACAC 180
TTACCTGTGG GCCAGTATTG TGAAGTGAGT CTGAGTTGTT TACACTGATG CCTTCCCTGC 240
CCACCACAAA TTGTGTACAT AGTCTTCAGA TGATACCACC CCTTTCCCCA GCTCCCAACC 300
20 AAGAGCTGGT TCTAGGCCCTG TGTATATATGT CATATTTAGC STTTTATAT ATGACCTTTG 360
ATTTCTGTGG TTTGTATTTT AGCACAGTGT ATGCACCTTC ATTTAAATAC ATCTGTGTGC 420
25 ATACAGATAC GCATATATGT GTGTGCGTAT GCATATATCT CTCATCTGTA GPTTCCAAGA 480
GPTCAGCTGA AGCAGATGGA GTCCTGCAGC CCAGGAGACA CCCTGCATCC CTGCTAATAG 540
TGTMTGCCAC AAGTATTAGT GAGTCTTCCT TATTAATATT TTCATTTTCAG AAGACTGAAG 600
30 CAAAGCTGAT AGTGTTTGCT GTTTCTTTGG CAGCTAAGTG AGGGTCTTGG GATGACTTGC 660
TGTGTTCTC AAGCTGCACT TTGGGGCCAT CTCGTCAGTA TTAGCCCCCT TTTTGCTTGG 720
35 TGGTACTCTG TCTGTGCTG TGTGTGTGTG TGATAGTCAC TCTTGCAATG CTTCCATGTC 780
TGGTTTGTGG CATTGTGGGA TAAGGTGCTG AAGCCAGAGC ATTTGCAGTT TGTTTGAGGC 840
CTCGTTGCCA ATGATAGATC ACTCCTGTTG ACCTGGTATG TCTGCTTGCT TGCTGCTTTT 900
40 CCTTGCTTTC TCTTGGAAGA GGAAAGGACT CTGGTCAGGC CCAGGCTGAG TGAGATGAGC 960
TGCAGCTGGC TCATGGCCTT CTTAGAGCAG AGAGAGGAGT ATGTCATTTT ACTAAGTTCC 1020
45 TAAACAAACA TTTATGCAGG CAACACTCCT TGCAATCCA GAAACTGAGG CACAATAGGG 1080
TTATGACTTG CTCAAGAATA TGTAGCTGCT AGGGGGTAAA TCAAGGCATC ACAATTTCTG 1140
TTCAGCGGGC AGGAATAGGC TGTGAATTGC TAGCACTTTT TTTTTTTAAG CAATTACTTT 1200
50 TTGACTTGTT CCTCTGAAAG TGCAAGAGGC GTACACCTTT CCCAAATGTA GACTAGAATC 1260
TGCAGGATGC CACCCACTGT ATAGTTCTGC TTTCCAGAG AGGAAGAACT TTTAGAAACC 1320
55 AAATGATCTT AATTGTTATT GCCCACCCTT GGCTTTTCCG GGTAGAAAAT TCACAGTAGG 1380
AATGATTGTT AAGAGAGAGT GCTTGAACC ATGGGTTAAC AGGAAAGGCT ACCTAAGTTC 1440
ACATATCTGC AACCAGAGCA GCCACCAAGC ATTACTTAGC AGCAGGAAAA TGATTGTATT 1500
60

TGAGTTCCTG TGTGTCCAAA ACTGAGGCAC CATGTTCTTT GAAAACATGC CACCTCAAGG 1560
 CTGGGCGCGG TGGCTCACAC CTGTAATCCC AGCAYTTTGG GGAGGCCSAG GCGGGGCGG 1620
 5 KTTTACCGGG GGTC 1634

10 (2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

20 TTCCCCCAG GTTGGCTTCC TTCGATTCCT TTTCTTGGTA TCAACGTTTG ATTGGAAGAA 60
 CAACCCCTC TTTGTCAACC TCAATAATGA GCTCACTGTG GAGGAGCAGC TCGGGCACAG 120
 CTCMCCGTYA TGGTCATTGT TACCCCCCAA GACCGCAAAA ACTCTGTGTG GACACAGGAT 180
 25 GGACCCTCAG CCCAGATCCT GCAGCAGCTT GTGGTCCTGG CAGCTGAAGC CCTGCCCATG 240
 TTAGAGAAGC AGCTCATGGA TCCCCGGGGA CCTGGGGACA TCAGGACAGT GTTCCGGCCG 300
 30 CCCTTGGACA TTTACGACGT GCTGATTGCG CTGTYTCCTC GCCATATCCC GCGGCACCGC 360
 AGGCTTGTGG ACTCGCCAGY TGCCTCCTTC TGCCGGGGCC TGCTCAGCCA GCCGGGGCCC 420
 TCATCCCTGA TGCCCGTGCT GGGTNATGAT CCTNCTCAGC TCTATCTGAC GCAGCTCAGG 480
 35 GAGGCCTTTG GGGATCTGGC CCTTTTCTTC TATGACCAGC ATGGTGGAGA GGTGATTGGT 540
 GTCTCTTGA AGCCCAACAG CTTCCAGCCG CAGCCCTTCA AGGCCTCCAG CACAAAGGGG 600
 40 CGCATGGTGA TGTCTCGAGG TGGGAGCTA GTAATGGTGC CCAATGTTGA AGCAATCCTG 660
 GAGGACTTTG CTGTGCTGGG TGAAGGCCTG GTGCAGACTG TGGAGGCCCG AAGTGAGAGG 720
 TGGACTGTGT GATCCAGCT CTGAGCAAG CTGTAGACGG ACAGCAGGAC AITGGACCTC 780
 45 TAGAGCAAGA TGTCAGTAGG ATGACCTCCA CCCTCCTTGG ACATGAATCC TCCATGGAGG 840
 GCCTGCTGGC TGAACATGCT GAATCATCTC CAACAAAACC CAGCCCCAAC TTTCTCTCTG 900
 50 ATGCTCCAGC ATTGGGGCAG GGGCATGGTG GCCCATGTAG TCTCTGGGC CTCACCATCC 960
 CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA GGAAGTGAAC CCAGGAGATC CATCCACCTA 1020
 TTAGCCCTGG GCCTGGACCT CCCTGCGATT TCCCACTCCT TTCTTAGTCT TCTTCCAGAA 1080
 55 ACAGAGAAGG GGATGTGTGC CTGGGAGAGG CTCTGTCTCC TTCCTGCTGC CAGGACCTGT 1140
 GCCTAGACTT AGCATGCCCT TCACTGCAGT GTCAGGCCCT TAGATGGGAC CCAGCGAAAA 1200
 60 TGTGGCCCTT CTGASTCACA TCACCGACAC TGAGCAGTGG AAAGGGGCTA TATGTGTATG 1260

AATAGACCAC ATTGAAGGAG CACAATGCCC TCCTGTGTTG ATGCCACTTC CCAGGGTGGA 1320
 GACAGTGGAA AAGAACCAG GACAGGAAAG GATTGGGTAG GTGAAGGGGT CAGGGGACTG 1380
 5 GTAGTCACCC AATCTTGGAG AGGTGCAAAA AGCACTGGGG GCTACCCGTT AGCTGCATCT 1440
 GCCCTGGCTG TTTGCCCGTT CATGTCACAA ACTGCCACTA CTATGTACCT GCAGTGGGGT 1500
 10 TGCAGAGATG GGGGAGACTC AAGTCTTACT CCCCAGGAGC TCCCAGGGCC CAAGGAGGAG 1560
 AATGCTGCCT CCTTTCAGTC TGGTCTACAC CCACTTTCTG GTAGCCTCTC TGCTTCCTGT 1620
 AATTCTGGCT GTTTTCCAG ACTCAGCTCA AATAGTGCCC CTCCTTAAGC CCATCCCTCG 1680
 15 CCCCCAGCCT GAGGTGATCT TTCCCTCCTC TGAATATTA GAGCAGTTAC TGTCTGTCTA 1740
 GTTCGTTTGG CAGGCACACA CAGTGGCATA AATTCTATTG TTTTGAAGTC TGATT 1795
 20

(2) INFORMATION FOR SEQ ID NO: 286:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 858 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCTGCTTTCTG GTGCTGCGTG TACTGCTGGG CGGCTTCTTC GCGCTCGTGG GGTGGCCAA 60
 35 GCTCTCGGAG GAGATCTCGG CTCCAGTTTC GGAGCGGATG AATGCCCTGT TCGTGCAGTT 120
 TGCTGAGGTG TTCCCGCTGA AGGTATTTGG CTACCAGCCA GATCCCTGA ACTACCAAAT 180
 AGCTGTGGGC TTTCTGGAAC TGCTGGCTGG GTTGCTGCTG GTCATGGGCC CACCGATGCT 240
 40 GCAAGAGATC AGTAACCTGT TCTTGATTCT GCTCATGATG GGGGCTATCT TCACCTTGGC 300
 AGCTCTGAAA GAGTCACTAA GCACCTGTAT CCCAGCCATT GTCTGCCTGG GGTTCCTGCT 360
 45 GCTGCTGAAT GTCGGCCAGC TCTTAGCCCA GACTAAGAAG GTGGTCAGAC CCACTAGGAA 420
 GAAGACTCTA AGTACATTCA AGGAATCCTG GAAGTAGAGC ATCTCTGTCT CTTTATGCCA 480
 TGCAGCTGTC ACAGCAGGAA CATGGTAGAA CACAGAGTCT ATCATCTTGT TACCAGTATA 540
 50 ATATCCAGGG TCAGCCAGTG TTGAAAGAGA CATTTTGTCT ACCTGGCACT GCTTTCTCTT 600
 TTTAGCTTTA CTA CTCTTTT GTGAGGAGTA CATGTTATGC ATATTAACAT TCCTCATGTC 660
 55 ATATGAAAAT ACAAATAAG CAGAAAAGAA ATTTAAATCA ACCAAAATTC TGATGCCCCA 720
 AATAACCACT TTTAATGCCT TGGTGTAAGT ATACCTCTGA ACTTTTTTCT GTGCCTTTAA 780
 ACAGATATAT ATTTTTTTT AATGAAAATA AAACCATATA TCCTATTTTA TTTCTCCTT 840
 60

TTAAACCTT ATAACTA

858

5

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 915 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

20

GAATTCGGCA CGAGCGCGGC CATGGCGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC 60

GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCTCGGAGG AGATCTCGGC TCCAGTTTCG 120

GAGCGGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCCTGAA GGTATTTGGC 180

TACCAGCCAG ATCCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAAGT GCTGGCTGGG 240

25

TTGCTGCTGG TCATGGGCCC ACCGATGCTG CAAGAGATCA GTAACCTGTT CTTGATTCTG 300

CTCATGATGG GGGCTATCTT CACCTTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360

CCAGCCATTG TCTGCCTGGG GTTCCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCCAG 420

30

ACTAAGAAGG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480

AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540

ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGGT CAGCCAGTGT TGAAAGAGAC 600

35

ATTTTGTCTA CCTGGCACTG CTTTCTCTTT TTAGCTTTAC TACTCTTTTG TGAGGAGTAC 660

ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720

40

TTTAAATCAA CCAAATCTT GATGCCCCAA ATAACCACTT TTAATGCCTT GGTGTAAGTA 780

TACCTCTGAA CTTTTTCTG TGCCTTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840

45

AACCATATAT CCTATTTTAT TTCCTCCTTT TAAACCTTA TAACTATAA MAAAAAAAAA 900

AAAAAAAAAA CTCGA 915

50

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 1517 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

	CCTTGTGGCA ACTAGTGGGT CCCCCGGGCT GCAGNAATTC GGGCAGTGGT TCTGNGTCTG	60
	AAGATACTCT GAGTTCCTCT GAGAGATCCA AAGGCTCCGG GAGCAGACCC CCAACCCCCA	120
5	AAAGCAGCCC TCAGAAGACC AGGAAGAGCC CTCAGGTGAC CAGGGGTAGC CCTCAGAAGA	180
	CCAGCTGTAG CCCTCAGAAG ACCAGGCAGA GCCCTCAGAC GCTGAAGCGG AGCCGAGTGA	240
	CCACCTCACT TGAAGCTTTG CCCACAGGAC AGTGCTGACA GACAAGAGTG GGCGACAGTG	300
10	GAAGCTGAAG TCCTTCCAGA CCAGGGACAA CCAGGGCATT CTCTATGAAG CTGCACCCAC	360
	CTCCACCCTC ACCTGTGACT CAGGACCACA GAAGCAAAAG TTCTCACTCA AACTGGATGC	420
15	CAAGGATGGG CGCTTGTTC A TGAGCAGAA CTCTTCCAG CGGGCCGCCA AGCCTCTGCA	480
	AGTCAACAAG TGAAGAAGC TGTACTCGAC CCCACTGCTG GCCATCCCTA CCTGCATGGG	540
	TTTCGGTGT T CACCAGGACA AATACAGGTT CTGGTGTGA CCCAGCCTGG GGAGGAGCCT	600
20	TCAGTCGGCC CTGGATGTCA GCCCAAAGCA TGTGCTGTGC AGAGAGGTCT GTGCTGCAGG	660
	TGGCCTGCCG GCTGCTGGAT GCCCTGGAGT TCCTCCATGA GAATGAGTAT GTTCATGGAA	720
25	ATGTGACAGC TGAATAATC TTTGTGGATC CAGAGGACCA GAGTCAGGTG ACTTTGGCAG	780
	GCTATGGCTT CGCNTTCCGC TATTGCCCAA GTGGCAAACA CGTGGCCTAC GTGGAAGGCA	840
	GCAGGAGCCY TCACGAGGGG GACCTTGAGT TTCATTAGCA TGGACCTGCA CAAGGGATGC	900
30	GGGCCCTCCC GCCGCRGYGA CCTCCAGAGC CTGGGYTAMT GCATGCTGAA GTGGYTCTAM	960
	GGGTTTCTGC CATGGACAAA TTGCCTTCCA AMAMTGAGGA CATCATGAAG CAAAAACAGA	1020
35	AGTTGCCTTG GGATTCAIT TTAATGTAAGC TKGACTTTGT CATGCCAGAA ACAAGGCTCG	1080
	GTCACCGTCA GCAGTTTGCA GTTTTCCACC TCCWCCAGT TCCTCCGTGT GGTTGACCCA	1140
	GATATCTCCG TTATGCAGCC GCCTCCGGGG GACCACCTCC CTCCTTTTGA GTCAGCCACA	1200
40	GACAGCCTAC TTGACGGCCC CGCTGGCCCC CACATTCCAC TGAAGTGTGC GGATGCCACA	1260
	GTGACCCCTC CTCAGGCACA GCATGACCTC CTGAAGTCGA GCCTGCTTGC TTTGAACCTA	1320
45	CCAGTTAAAA TCTCCTCAA ATGTTTGGAT ACCGCCCAT TGGCCCTCAC AGCCACGAGC	1380
	TCCCTGACCA GTGTGCGTGT GTGTGTGTGT GTGTGTCTGT GTGTGTGCTT GGGACGGGTG	1440
	GGGAGGTCAC CTTTGGGTGT GCGGTGTGCC CCCAGGACCT GTAAGTAATA AAATCTTTAT	1500
50	TTCCAAAAA AAAAAA	1517

55

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3865 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

5	TGGAGGGGGG GAGCTTCCTT GAGCAGTGGG CCCAGGCCCTG GCCCTCCACA CTTCAATTCTC	60
	TGACCTTTCT CTCTCCTCAT TTCGGTGCAT GTCTTTCTG CAGCTGCCTT TCAGCACAGG	120
10	TGGTTCCACT GGGGGCAGCT AACGCTGAGT GACAAGGATG GGAAGCCACA GGTGCATTTT	180
	ACTCAAGTCT TCTCTAGTCA ATGAGGGGCA CCCAGTGCTT CTAGGGCAGG CTGGGTGGTG	240
	GTCCCTTAGG TATCAGCCTC TCTTACTGTA CTCTCCGGGA ATGTTAACCT TTCTATTTTC	300
15	AGCCTGTGCC ACCTGTCTAG GCAAGCTGGC TTCCCCATG GCCCTGTGG GTCCACAGCA	360
	GCGTGGCTSC CCCCCAGGGC CACCGCTTCT TTCTTGATCC TCTTTCTTTC ACAGTGACTT	420
20	GGGCTTGAGT CTGGCAAGGA ACCTTGCTTT TAGCTTCACC ACCAAGGAGA GAGGTTGACA	480
	TGACCTCCCC GCCCCCTCAC CAAGGCTGGG AACAGAGGGG ATGTGGTGAG AGCCAGGTTT	540
	CTCTGGCCCT CTCCAGGGTG TTTTCCACTA GTCACTACTG TCTTCTCCTT GTAGCTAATC	600
25	AATCAATATT CTTCCCTTGC CTGTGGGCAG TNGGAGAGTG CTGCTGGGTG TACGCTGCAC	660
	CTGCCCACTG AGTTGGGGAA AGAGGATAAT CAGTGAGCAC TGTCTGCTC AGAGCTCCTG	720
30	ATCTACCCCA CCCCCTAGGA TCCAGGACTG GGTCAAAGCT GCATGAAACC AGGCCCTGGC	780
	AGCAACCCCTG GGAATGGCTG GAGGTGGGAG AGAACCTGAC TTCTCTTTCC CTCTCCCTCC	840
	TCCAACATTA CTGGAACCTC ATCCTGTTAG GATCTTCTGA GCTTGTTCCT CTGCTGGGTG	900
35	GGACAGAGGA CAAAGGAGAA GGGAGGGTCT AGAAGAGGCA GCCCTTCTTT GTCCTCTGGG	960
	GTAAATGAGC TTGACCTAGA GTAAATGGAG AGACCAAAAG CCTCTGATTT TTAATTTCCA	1020
40	TAAAATGTTA GAAGTATATA TATACATATA TATATTTCTT TAAATTTTGG AGTCTTTGAT	1080
	ATGTCTAAAA ATCCATTCCC TCTGCCCTGA AGCCTGAGTG AGACACATGA AGAAAACGT	1140
	GTTCATTTTA AAGATGTTAA TTAAATGATT GAAACTTGGC TGTGGCTACT GCTTCTTAAT	1200
45	GTGGGGGGGA CAGGGCAGTG GTCTGGCCCC ACATTTAGAA GGGAAAATGT TTTGCCTGCT	1260
	GCACACATTG GACCCAGTA TGGGCCTCTT CTGCCTAGTA CTGCCAAAGG GACTGTTAAG	1320
50	GTGTCTTGTC CATCTTCTAC CCCCCACCCC CCATTACGGG TAAAGGRAAC CCCAGACTAG	1380
	GTGAGGGGCC AGCAGCTGCC TCACATTGTG TTCTCTCCTG AGATGGTCCA GCTCACATCC	1440
	AGACACCTTG TTCAGACATT TTATTTGAAT TTATGACAGT GATGGGGATT TGACTGAGAT	1500
55	GCCTTATGGA GAAGTACCCC ACCCTCTATG AAGACAGAAT CACTCTCTGC CATTCATTCT	1560
	GCCTGATGCT AACAACACGC AGCTGATTTA GGGAGTGTCC CAGCCTAGCT GGATCAAGGG	1620
60	AAATTCAGG AGCCCTGGGG CAGGCCCTGG NCCCCAGTGC CAAGCCTCAG AGTAAGCAGA	1680

	CATTGGGAAA GTTGCCAACC ACTTGGTAGA CCACTAGGTT CTCTGTTTTC CCTTCCCTTT	1740
5	CCTTTTCAAA TCCCACAGTT TCCTGTTGGG GAGAAGCTGT AATTAGCCTA GTCCAGGTAC	1800
	CAGATCCAG CTAGGGGCGC AGCTGNCTTG GATAACTCCA AGAAAACCTG GGCACCASTA	1860
	TTTTTCCAAT TATAAGGACT GTGGCATAAA TTTTAAATG AGTTATATTG AAACCAGATT	1920
10	TCTCCAGCTG CCAAGGGAAG AAGGTAGGGC TGGACTCCCT GCTGTGGCCC AGCCCTTGTT	1980
	AGGGGTGGT CTCTCACTGC AGCCAGACAG GATGATCCTG GGTCTGGGG AGGGTAAGCT	2040
15	GCCCCTTGCC GAGTTCTGCA CCGAATAAAG AGTCCAAACC CGCTGCTTCC GTGCTCTGAG	2100
	AGATGGGTAA ATGGGTGATG GATGGAGCAG ACTGAAGAGA CAGCAGATGA CTCAGTGGTG	2160
	GAAGAAGGGG GGAAGATGCT GGGCTGGCTA GCTAATGTTT CCCCCTTTCA GCGATTTACA	2220
20	GGAAATGGAG CCCAGCTTGG TCATGAAGTT GGTTCGCTTC CACTGTGCGA TGCACTCCTC	2280
	AGAAATTTTG AAGTCAGCCT GCAACTTCTC GAAGACTTTC TTCTTGGGCT TGAGCTCCTC	2340
25	ATCTGGTTGG CCTTTTTCAT AGCCCTTCAC AAACACGTGC TCACCAGGAG CAGAGCCTGC	2400
	CGGAGGGTCC AGAGGTTCAA CTGGCGGTTT ATCCCTTCTA TAGAAGCACA CAGAAGCATG	2460
	CCTTGGGACT CGACTCCTCT CATCTTCTGG GGTTCAGGT TGCACAGCAC CACTACCAGC	2520
30	CTGTCTGCA GTTCTCTCTT GGGCACGAAC TGTACCAGGC CGCTCACCAC AGTCCGTGGT	2580
	TCAGCTTCCC CCACGTCAAT CTCTCTTACA TACAGGCTGT CTGCATCTGG GTGCTTCTCC	2640
35	ACAGTGATGA TTTTCCCCAC ACGGATATCC AGCCGGGATG GGATGACCTC CTCTGGTTCT	2700
	GAATTCCTGG CAGGCCCTTG GCCATTGGCT TCTGCTTTGA GGGATCTGGG TAGGCAGCGC	2760
	TGGCCAGTTT TTTCAGGCA GGGGTATTAA ACTTTTCCCG GATTGGATCC AGCAACTTGT	2820
40	TCAGTGCGAC TTCAACAGAA TTCTTCAGGT CTCCAGGATG TACAACCTCA GCAGCAAAGT	2880
	CCTTTTCCAG GTCCACGTAA GCTGTGTAGG TTTTGTTC ACCCCATTTC TCATCTCGTA	2940
45	GGATCACAAA CTCGGACTTA AGGGGAAAAA GGACATGCTT GATGAAGGAC AGAACCCCAT	3000
	TGTTCTCCAC ATTTCTTGGC TCACAGAAGG CCTTCTTCAG TTTTTCCTTC ACATCTCTCT	3060
	TCCGATCAAG GAGATCAATC TTGGACTCCT CTTCTGAAGA GCTCATTTTG CTGCCTGTTA	3120
50	ATCCTGGAAC CATAGGATTC ATCAGATGGA CCCGTTTGA ATAGCCAAGT GCAGGGAGGT	3180
	ACTTCTCTGC AAAGGTGAAA ATCTTTCTCT GATCAATGCC TCCAAATTGG GCATCTACTT	3240
55	TTAAATACTC TTCATCCAAA GCCTGCAGTC CGGGGTATAA GAGGCCACTC AGCAAAGGGT	3300
	GCTCCACCTG CTTTACCACC TCAGCTCCAG CCTTCTTGA ATCGTGCTGT GTGACCACGG	3360
	AGGAGAGTCT GTACACATCT AGTGTGTA CTCTGCTGAG CTGGTAATCA GTGCCTTTGA	3420
60	TGAACMTGAG CTTCTCCAAG GGCACACCAA TGCTCTCCAG CATTGCTTTG ATCACATTCT	3480

CATAGTAACT GACTCGGAGT TCTAGAAGTT CCCATGGGGC TTTCATGTTA TCCAGGTATG 3540
CGTGGAGGTC CGCAAACAGA ATTGTTACCT CACACCCTGC CTTTAAGAAG TCTGCAATCT 3600
5 TTGACATGGG CACAAAGTAA GCCACATGTG GTTTGCCCCGTT GGTGCGCGTT CCCCAGTAAA 3660
TTMTAAGTTC CCGCTCCTTC AGTATCTCCT TCAGCTTCTC TTCCCCCAGA ACCTCCTGCA 3720
10 GGTTCGCGGT GATAAGGTGC AGTTTCTCTT CAGGCTGGG AGCGTCCCC ATGGTCCGCT 3780
ACCCCTGCTT CCCCCGCTCA GCGCGGCACC AGAGCCCCCTT CCTGGGTACG CGTCGCCGCC 3840
GCGTGCCGGG AACTGTCACG CGAGT 3865
15

(2) INFORMATION FOR SEQ ID NO: 290:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1910 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

AGGGAGAGGA GGAGAGGGGG TCTGCGCGCG GCCCTACCC AGAAGCCAGC GGACGGCAGC 60
30 ACGGAGTGGG CTGTCCCCGA GCCCAGCCCC GAGCGAGCCC CCCCCCGCC CCGMAGGAC 120
GCGCCTYCCA GCCAGCCCGA CTCCTAGGAG GAGGGGAGGC GGGAAAGCAG CTCGAAGCCTC 180
35 ACCCACCGCC CTGCCCCCAG CCCC GCCACT CCCAGGCTCC TCGGGACTCG GCGGTCCTC 240
CTGGGAGTCT CGGAGGGGAC CGNCTGTGCA GACGCCATGG AGTTGGTGCT GGTCTTCCTC 300
TGCAGCCTGC TGGCCCCCAT GTTCCTGGCC AGTGCAGCTG AAAAGGAGAA GGAAATGGAC 360
40 CCTTTTCAIT ATGATTACCA GACCCTGAGG ATTTGGGGAC TGGTGTTCGC TGTGGTCCTC 420
TTCTCGGTG GGATCCTCCT TATCCTAAGT CGCAGGTGCA AGTGCAGTTT CAATCAGAAG 480
45 CCCCCGGCCC CAGGAGATGA GGAAGCCCAG GTGGAGAACC TCATCACCGC CAATGCAACA 540
GAGCCCCAGA AAGCAGAGAA CTGAAGTGCA GCCATCAGGT GGAAGCCTCT GGAACCTGAG 600
GCGGCTGCTT GAACCTTTGG ATGCAAATGT CGATGCTTAA GAAAACCGGC CACTTCAGCA 660
50 ACAGCCCTTT CCCCAGGAGA AGCCAAGAAC TTGTGTGTCC CCCACCCTAT CCCCTCTAAC 720
ACCATTCCTC CACCTGATGA TGCAACTAAC ACTTGCCTCC CCACTGCAGC CTGCGGTCTT 780
55 GCCCACCTCC CGTGATGTGT GTGTGTGTGT GTGTGTGTGT GACTGTGTGT GTTTGCTAAC 840
TGTGGTCTTT GTGGCTACTT GTTTGTGGAT GGTATTGTGT TTGTTAGTGA ACTGTGGACT 900
CGCTTTCCCA GGCAGGGGCT GAGCCACATG GCCATCTGCT CCTCCCTGCC CCGTGCGCCC 960
60

TCCATCACCT TCTGCTCCTA GGAGGCTGCT TGTGCCCCGA GACCAGCCCC CTCCCCTGAT 1020
TTAGGGATGC GTAGGGTAAG AGCACGGGCA GTGGTCTTCA GTCGTCTTGG GACCTGGGAA 1080
5 GGTTCGACG ACCTTGTCAT CATCTCTCAT GGACTCCTTT CACTCCTTTA AAAAAAACCT 1140
TGCTTCCTTA TCCCACCTGA TCCCAGTCTG AAGGTCTCTT AGCAACTGGA GATACAAAGC 1200
AAGGAGCTGG TGAGCCGAGC GTTGACGTCA GGCAGGCTAT GCCCTTCCGT GGTTAATTTT 1260
10 TTCCCAGGGG CTTCCACGAG GAGTCCCCAT CTGCCCCGCC CCTTCACAGA GCGCCCCGGG 1320
ATTCACAGCC CAGGGCTTCT ACTCTGCCCC TGGGAATGT GTCCCCTGCA TATCTTCTCA 1380
15 GCAATAACTC CATGGGCTCT GGGACCCCTAC CCCTTCCAAC CTTCCTGCT TCTGAGACTT 1440
CAATCTACAG CCCAGTCAT CCAGATGCAG ACTACAGTCC CTGCAATTGG GTCTCTGGCA 1500
GGCAATAGTT GAAGGACTCC TGTTCGGTTG GGGCCAGCAC ACCGGGATGG ATGGAGGGAG 1560
20 AGCAGAGGCC TTTGCTTCTC TGCCTACGTC CCCTTAGATG GGCAGCAGAG GCAACTCCCG 1620
CATCCTTTGC TCTGCCGTGC GGTGGTCAGA GCGGTGAGCG AGGTGGGTTG GAGACTCAGC 1680
25 AGGCTCCGTG CAGCCCTTGG GAACAGTGAG AGGTGAAGG TCATAACGAG AGTGGGAACT 1740
CAACCCAGAT CCGCCCCCTC CTGTCTCTG TGTTCCTCGG GAAACCAACC AAACCGTGG 1800
CTGTGACCCA TTGCTGTTCT CTGTATCGTG ATCTATCCTC AACAACAACA GAAAAAAGGA 1860
30 ATAAATATC CTTGTGTTTCM TAAAAAATAA AAAAAAATAA AGGGGGGGGG 1910

35

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 3276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

45

GCGACCGTCG TTTGAGTCGT CGCTGCCGCT GCCGTGCCA CTGCCACTGC CACCTGCGG 60
ATCAGGAGCC AGCGTTGTTC GCCCAGCGCC TCGCTGCCG TGGGAGGAAG CGAGAGGGAA 120
50 GCGCTTGCG GGTTCGTGCG CGCTGCTCGC CCACCGCCTG GAAGAGCCGA GCCCCGGCCC 180
AGTCGGTGC TTGCCACGCG TCGTAGCCGT TACCGCGGG CCGCCACAGC CGCCGGCCCG 240
GAGAGGCGCG CGCCATGGCT TCTGGAGCCG ATTCAAAAGG TGATGACCTA TCAACAGCCA 300
55 TTCTCAAACA GAAGAACCGT CCAATCGGT TAATTGTTGA TGAAGCCATC AATGAGGACA 360
ACAGTGTGGT GTCCTGTGCC CAGCCCAAGA TGGATGAATT GCAGTTGTTC CGAGGTGACA 420
60 CAGTGTGCT GAAAGGAAAG AAGAGACGAG AAGCTGTTG CATCGTCCTT TCTGATGATA 480

	CTTGTTCTGA TGAGAAGATT CGGATGAATA GAGTTGTTG GAATAACCTT CGTGACGCC	540
	TAGGGGATGT CATCAGCATC CAGCCATGCC CTGATGTGAA GTACGGCAA CGTATCCATG	600
5	TCCTGCCCCAT TGATGACACA GTGGAAGGCA TTAAGGTAA TCTCTTCGAG GTATACCTTA	660
	AGCCGTAATT CCTGGAAGCG TATCGACCCA TCCGGAAGG AGACATTTTT CTTGTCCGTG	720
10	GTGGGATGCG TGCTGTGGAG TTCAAAGTGG TGGAAACAGA TCCTAGCCCT TATTGCATTG	780
	TTGCTCCAGA CACAGTGATC CACTGCGAAG GGGAGCCTAT CAAACGAGAG GATGAGGAAG	840
	AGTCCTTGAA TGAAGTAGGG TATGATGACA TTGGTGGCTG CAGGAAGCAG CTAGCTCAGA	900
15	TAAAGGAGAT GGTGGAAGT CCCCTGAGAC ATCCTGCCCT CTTTAAGGCA ATTGGTGTGA	960
	AGCCTCCTAG AGGAATCCTG CTTTACGGAC CTCCTGGAAC AGGAAAGACC CTGATTGCTC	1020
20	GAGCTGTAGC AAATGAGACT GGAGCCTTCT TCTTCTTGAT CAATGGTCCT GAGATCATGA	1080
	GCAAATTGGC TGGTGAGTCT GAGAGCAACC TTCGTAAAGC CTTTGAGGAG GCTGAGAAGA	1140
	ATGCTCCTGC CATCATCTTC ATTGATGAGC TAGATGCCAT CGCTCCCAA AGAGAGAAAA	1200
25	CTCATGGCGA GGTGGAGCG CGCATTGTAT CACAGTTGTT GACCCTCATG GATGGCCTAA	1260
	AGCAGAGGGC ACATGTGATT GTTATGGCAG CAACCAACAG ACCCAACAGC ATTGACCCAG	1320
30	CTCTACGGCG ATTTGGTCGC TTTGACAGGG AGGTAGATAT TGGAAATTCCT GATGCTACAG	1380
	GACGCTTAGA GATTCTTCAG ATCCATACCA AGAACATGAA GCTGGCAGAT GATGTGGACC	1440
	TGGAACAGTA GCCAATGAGA CTCACGGGCA TGTGGGTGCT GACTTAGCAG CCCTGTGCTC	1500
35	AGAGGCTGCT CTGCAAGCCA TCCGCAAGAA GATGGATCTC ATTGACCTAG AGGATGAGAC	1560
	CATTGATGCC GAGGTATGA ACTCTCTAGC AGTTACTATG GATGACTTCC GGTGGGCCTT	1620
40	GAGCCAGAGT AACCCATCAG CACTGCGGGA AACCGTGGTA GAGGTGCCAC AGGTAACCTG	1680
	GGAAGACATC GGGGGCCTAG AGGATGTCAA ACGTGAGCTA CAGGAGCTGG TCCAGTATCC	1740
	TGTGGAGCAC CCAGACAAAT TCCTGAAGTT TGGCATGACA CCTTCCAAGG GAGTTCTGTT	1800
45	CTATGGACCT CCTGGCTGTG GGAAACTTT GTTGGCCAAA GCCATTGCTA ATGAATGCCA	1860
	GGCCAACTTC ATCTCCATCA AGGGTCCTGA GCTGCTCACC ATGTGGTTTG GGGAGTCTGA	1920
50	GGCCAAATGTC AGAGAAATCT TTGACAAGGC CGCCAAGCT GCCCCCTGTG TGCTATTCTT	1980
	TGATGAGCTG GATTGATTG CCAAGGCTCG TGGAGGTAAC ATTGGAGATG GTGGTGGGGC	2040
	TGCTGACCGA GTCATCAACC AGATCCTGAC AGAAATGGAT GGCATGTCCA CAAAAA	2100
55	TGTGTTTCATC ATTGGCGCTA CCAACCGGCC TGACATCATT GATCCTGCCA TCCTCAGACC	2160
	TGCGCTCTT GATCAGCTCA TCTACATCCC ACTTCCTGAT GAGAAGTCCC GTGTGCCAT	2220
60	CCTCAAGGCT AACCTGCGCA AGTCCCCAGT TGCCAAGGAT GTGACTTGG AGTTCTGGC	2280

TAAATGACT AATGGCTTCT CTGGAGCTGA CCTGACAGAG ATTTGCCAGC GTGCTTGCAA 2340
 GCTGGCCATC CGTGAATCCA TCGAGAGTGA GATTAGGCGA GAACGAGAGA GGCAGACAAA 2400
 5 CCCATCAGCC ATGGAGGTAG AAGAGGATGA TCCAGTGCCT GAGATCCGTC GAGATCACTT 2460
 TGAAGAAGCC ATGCGCTTTG CGCGCCGTTT TGTCAGTGAC AATGACATTG GGAAGTATGA 2520
 10 GATGTTTGCC CAGACCCTTC AGCAGAGTCG GGGCTTTGGC AGCTTCAGAT TCCCTTCAGG 2580
 GAACCAGGGT GGAGCTGGCC CCAGTCAGGG CAGTGGAGGC GGCACAGGTG GCAGTGATATA 2640
 CACAGAAGAC AATGATGATG ACCTGTATGG CTAAGTGGTG GTGGCCAGCG TGCAGTGAGC 2700
 15 TGGCCTGCCT GGACCTTGTT CCTGGGGGT GGGGGCGCTT GCCCAGGAGA GGGACCAGGG 2760
 GTGCGCCAC AGCCTGCTCC ATTCTCCAGT CTGAACAGTT CAGCTACAGT CTGACTCTGG 2820
 20 ACAGGGGGTT TCTGTTGCAA AAATACAAAA CAAAAGCGAT AAAATAAAAG CGATTTTCAT 2880
 TTGGTAGGCG GAGAGTGAAT TACCAACAGG GAATTGGGCC TTGGGCTATG CCATTCTGT 2940
 TGTAGTTGG GGCAGTGCG GGGACCTGTG TGGGGTGTGA ACCAAGGCAC TACTGCCACC 3000
 25 TGCCACAGTA AAGCATCTGC ACTTGACTCA ATGCTGCCCG AGCCCTCCCT TCCCCCTATC 3060
 CAACCTGGGT AGGTGGGTAG GGGCCACAGT TGCTGGATGT TTATATAGAG AGTAGGTTGA 3120
 30 TTTATTTTAC ATGCTTTTGA GTTAATGTTG GAAACTAAT CACAAGCAGT TTCTAAACCA 3180
 AAAAATGACA TGTGTAAAA GGACAATAAA CGTTGGGTCTN AAATGGGWRA AAAAAAAAAA 3240
 AAAAAAGGGG GGCCCCCTCTA AAGNCCANN CTTCGT 3276
 35

(2) INFORMATION FOR SEQ ID NO: 292:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1695 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

TTGCAATGGT TGAATTCCCC TCCTCACGCC AGCCTAGGAG AAGAAGTTCTG TAGTCCCAGA 60
 50 GGTGAGGCAG GAGCGGCAG TTTCTGGCGG GTGAGGGCGG AGCTGAAGTG ACAGCGGAGG 120
 CGGAAGCAAC GGTGGGTGGG GCGGAGAAGG GGGCTGGCCC CAGGAGGAGG AGGAAACCTT 180
 55 TCCGAGAAAA CAGCAACAAG CTGAGCTGCT GTGACAGAGG GGAACAAGAT GGCGGCGCCG 240
 AAGGGAGCCT CTGGGTGAGG ACCCAACTGG GGCTCCCGCC GCTGCTGCTG CTGACCATGG 300
 60 CCTTGGCCCG AGGTTGGGG ACCGCTTCGG CTGAAGCATT TGAATCGGTC TTGGGTGATA 360

CGGCGTCTTG CCACCGGGCC TGTCACTTGA CCTACCCCTT GCACACCTAC CCTAAGGAAG 420

AGGAGTTGTA CGCATGTCAG AGAGGTTGCA GGCTGTTTTT AATTGTGTCAG TTTGTGGATG 480

5 ATGGAATTGA CTTAAATCGA ACTAAATTGG AATGTGAATC TGCATGTACA GAAGCATATT 540

CCCAATCTGA TGAGCAATAT GCTTGCCATC TTGGTTGCCA GAATCAGCTG CCATTGCTG 600

10 AACTGAGACA AGAACAACCT ATGTCCCTGA TGCCAAAAAT GCACCTACTC TTTCTCTTAA 660

CTCTGGTGAG GTCATTCTGG AGTGACATGA TGGACTCCGC ACAGAGCTTC ATAACCTCTT 720

CATGGACTTT TTATCTTCAA GCCGATGACG GAAAAATAGT TATATTCCAG TCTAAGCCAG 780

15 AAATCCAGTA CGCACCACAT TTGGAGCAGG AGCCTACAAA TTTGAGAGAA TCATCTCTAA 840

GCAAAATGTC CTATCTGCAA ATGAGAAATT CACAAGCGCA CAGGAATTTT CTTGAAGATG 900

GAGAAAGTGA TGGCTTTTTA AGATGCCTCT CTCTTAACTC TGGGTGGATT TTAACCTACAA 960

20 CTCTGTCTCT CTCGGTGATG GTATTGCTTT GGATTTGTTG TGCAACTGTT GCTACAGCTG 1020

TGGAGCAGTA TGTTCCCTCT GAGAAGCTGA GTATCTATGG TGACTTGGAG TTTATGAATG 1080

25 AACAAAAGCT AACAGATAT CCAGCTTCTT CTCTTGTGGT TGTTAGATCT AAAACTGAAG 1140

ATCATGAAGA AGCAGGGCCT CTACCTACAA AAGTGAATCT TGCTCATCTT GAAATTTAAG 1200

CATTTTTCTT TTTAAAGACA AGTGAATAG ACATCTAAAA TTCCACTCCT CATAGAGCTT 1260

30 TTAAATGGT TTCATTGGAT ATAGGCCCTA AGAAATCACT ATAAATGCA AATAAAGTTA 1320

CTCAAATCTG TGAAGACTGT ATTTGCTATA ACTTTATGG TATTGTTTTT GTAGTAATTT 1380

35 AAGAGGTGGA TGTTGGGAT TGTATTATTA TTCTACTAAT ATCTGTAGCT ATTTGTGTTT 1440

TTGCTTTGGT TATTGTTTTT TTCCCTTTTC TTAGCTATGA GCTGATCATT GCTCCTTCTC 1500

ACCTCCTGCC ATGATACTGT CAGTTACCTT AGTTAACAAG CTGAATATTT AGTAGAAATG 1560

40 ATGCTTCTGC TCAGGAATGG CCCACAAATC TGTAATTTGA AATTTAGCAG GAAATGACCT 1620

TTAATGACAC TACATTTTCA GGAAGTAAA TCATTAAAA TTTATTTGAA TAATTAAAAA 1680

45 AAAAAAAAAA AANCT 1695

50 (2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

60 CACTTTCAGC AGTCCTTTGC TCTCTTTGCT TCTACCTCAA ATAGCCCCAG GAGTGGGCTT 60

	TAGTCTCCAA TATGGAGCAT CTCAAGCTTC TCCTGGGGGA TGGGGATTGG GATGGGCAGA	120
5	ATCTGTTTTG GWTCTCCGGG TTATTTCCAG TGGGTGTAAA AGCAGAGCTG GGCCTTTCCC	180
	TCTCTTATCC CTGAGGGTGG GTAAGAAGGA CTGTATCTAC ACCTGTTCTT CCCTACCTTC	240
	TCTTTTGTTA GGGAGGCCTC ATTCTAAGTT CCTCAAGAGA GTCCTTGGCT TAAAGCTGTA	300
10	GCAAGGGTGT GCTAGGTGGG GGAATTGGAG CAAAACCGTC GAGTAGGCAT GATACTGGTA	360
	TGGAGTGGGC CTGCAAAATC AGACAGAAAT GGCTTGAGAA GCCGCAGGGG AGCATGCCTG	420
15	TCTCTCAGTG ATAGAGTATG GGAGGGACCT CCCTAGCTTG GAAAATGAGA ATTGAAGGGG	480
	TTATGAACAA ATAGGATGCC TAGTTGAGGA TGTTCCTAAA GTTTTGTCCA ATCTTATCAT	540
	TAGTAGATTT TATAAGCCAC AGAGACAAAC CAGAAACGGA ATAATGTTAC TTTGGATGCT	600
20	TTATTTTTTT GTTCTAGGTG TGGCTTTGTA CATGCAGAAG AATGCTATAT GCTGCACATT	660
	TTGCCTTTAA AGTCTTACGA CTTTCCCAT TTTAGTCTAA TGGGAAGATA CAGATGTGCA	720
25	AGTCTGCTTT TTTGTTTTTT GTTATTATTT TTTTTTTTTT GCTCTGTGTT ATGGACATTT	780
	TCAGACATGC ACAGAAGTGG AGAGGATGGT CCTTGGACCC MATGTGTCCA TCACCTAGCT	840
	GCATCACTTA TCAGCTATGG TCAACCTGGT TTCATCTGTA TCTCTCTCTT TTCACCTGTA	900
30	TTGTTTATTG AAAATCCAAG AACTATGCC AATGCAACCG TGACTACTTT GGGAGATTGG	960
	TAGTCTCTTT TGATGGTGAT AGTGATGGGG TGCACTATCA TAATCACATC AGGTCTGCTT	1020
35	TTTGCTTTTA ATGTAACTA ATGAAGTTCC AGAGATGGGC CTTAGAAATG TGTTTTAAGA	1080
	ATTAACAAGG AGTCTCAAAA AGAAATGAGA GGGATGCTTC CTTTNCCTT GCATCTACAA	1140
	AACMAGAGAG AGACTGTTCT GTTGTAATAAC TCTTTCAAAA ATTCTGATAT GGTAAGGTAC	1200
40	TTGAGACCTT TCACCAGAAT GTCAATCTTT TTTCTGTGT AACATGGAAA CTGTGTGAC	1260
	CATTAGCAAT GTTATCAGCT TGTACTGGTC TCATAACTCT GGTTTTGGAA GAATAATTTG	1320
45	GAAATTGTTG CTGTGTTCTG TGAAAATAAC CTCCCCAAAA TAATTAGTAA CTGGTTGTTT	1380
	TACTTGGTAA TTTGACACCC TGTTAATAAC GCAATTATTT CTGTGTTCTT AAACAGTATA	1440
	AATAGTTGTA AGTTTGCATG CATGATGGAA AAATAAAAAC CTGTATCTCT GTTAAAAAAA	1500
50	A	1501

55 (2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

5	TGANTGTGGT CCCGGGTGCN GATTGGCAGN GCCTCCGCCG CGGCTCGTGG TTGTCCCGCC	60
	ATGGCACTGT CGCGGGGGCT GCCCGGGGAG CTGGCTGAGG CGGTGGCCGG GGGCCGGGTR	120
10	CTGGTGGTGG GGGCGGGCGG CATCGGCTGC GAGCTCCTCA AGAATCTCGT GCTCACCGGT	180
	TTCTCCCA CA TCGACCTGAT TGATCTGGAT ACTATTGATG TAAGCAACCT CAACAGACAG	240
	TTTTTGTTC AAAAGAAACA TGTGGAAGA TCAAAGGCAC AGGTTGCCAA GGAAAGTGTA	300
15	CTGCAGTTT ACCCGAAAGC TAATATCGTT GCCTACCATG ACAGCATCAT GAACCTGAC	360
	TATAATGTGG AATTTTCCG ACAGTTTATA CTGGTTATGA ATGCTTTAGA TAACAGAGCT	420
20	GCCCGAAACC ATGTTAATAG AATGTGCCTG GCAGCTGATG TTCTCTTAT TGAAAGTGGA	480
	ACAGCTGGGT ATCTTGACA AGTAACTACT ATCAAAAAGG GTGTGACCGA GTGTTATGAG	540
	TGTCATCCTA AGCCGACCCA GAGAACCCTT CCTGGCTGTA CAATTCGTAA CACACCTTCA	600
25	GAACCTATAC ATTCATCGT TTGGGCAAAG TACTTGTTC ACCAGTTGTT TGGGGAAGAA	660
	GATGCTGATC AAGAAGTATC TCCTGACAGA GCTGACCTG AAGCTGCCTG GGAACCAACG	720
30	GAAGCCGAAG CCAGAGCTAG AGCATCTAAT GAAGATGGTG ACATTAAACG TATTTCTACT	780
	AAGGAATGGG CTAAATCAAC TGGATATGAT CCAGTTNAAA CTTTTTACCA AGCTTTTTAA	840
	AGATGACATC AGGTATCTGT TGACAATGGA CAACTATGG CGGAAAAGGA AACCTCCAKT	900
35	TCCGTGGAC TGGGCTGAAG TACAAAGTCA AGGAGAAGAA ACGAATGCAT CAGATCAACA	960
	GAATGAACCC CAGTTAGGCC TGAAAGACCA GCAGTTCTA GATGTAAAGA GCTATGCACG	1020
40	TCCTTTTTC AAGAGCATCG AGACTTTGAG AGTTCATTTA GCAGAAAAGG GGGATGGAGC	1080
	TGAGCTCATA TGGGATAAGG ATGACCCATC TGCAATGGAT TTTGTCACCT CTGCTGCAA	1140
	CCTCAGGATG CATATTTTCA GTATGAATAT GAAGACTAGA TTTGATATCA AATCAATGGC	1200
45	AGGGAACATT ATTCTGCTA TGCTACTAC TAATGCAGTA ATTGCTGGGT TGATAGTATT	1260
	GGAAGGATG AAGATTTTAT CAGGAAAAAT AGACCACTGC AGAACAATTT TTTTGAATAA	1320
50	ACAACCAAAC CCAAGAAAGA AGCTTCTTGT GCCTTGTGCA CTGGATCCTC CCAACCCCAA	1380
	TTGTTATGTA TGTGCCAGCA AGCCAGAGGT GACTGTGCGG CTGAATGTCC ATAAAGTGAC	1440
	TGTTCTCACC TTACAAGACA AGATAGTGAA AGAAAAATTT GCTATGGTAG CACCAGATGT	1500
55	CCAAATTGAA GATGGGAAAG GAACAATCCT AATATCTTCC GAAGAGGGAG AGACGGAAGC	1560
	TAATAATCAC AAGAAGTTGT CAGAATTGG AATTAGAAAT GGCAGCCGGC TTCAAGCAGA	1620
60	TGACTTCTC CAGGACTATA CTTTATGAT CAACATCCTT CATAGTGAAG ACCTAGGAAA	1680

	GGACGTTGAA TTTGAAGTTG TTGGTGATGC CCCGGAAAAA GTGGGGSCCA AACAAAGCTGA	1740
	AGATGCTGCC AAAAGCATAA CCAATGGGCA GTGATGATGG AGCTCAGCCC TCCACCTCCA	1800
5	CAGCTCAAGA GCAAGATGAC GTTCTCATAG TTGATTGCGA TGAAGAAGAT TCTTCAAATA	1860
	ATGCCGACGT CATGAAGAAG AGAGAAGCCG CAAGAGGAAA TTAGATGAGA AAGAGAATCT	1920
	CAGTGCAAAG AGGTACGTA TAGAACAGAA GGAAGAGCTT GATGATGTCA TAGCATTAGA	1980
10	TTGAACAGAA ATGCCTCTAA ACAGAACCCT CTTACTATTT AGTTTATCTG GGCAGAACCA	2040
	GATTGTTATG TCCTTTGTTC CAAAGGAAA AAATTGACAG CAGTGACTTG AAAATGATTC	2100
15	TGCTCCCTTT GAAAGCATTC ATTTTGCTAG AACTGTTAGA CACATTGCAG TATGCTGTAT	2160
	TGAAAGTAGG AATATAGTTT TAAAAACCCT TTGAACAAAG TGTGTGCATA ACCAGTCATG	2220
	AGATAAAACA ACACAATGCA TGTTCCTTTT TTAATGTAAA TACCCTTAGG TATCATTAAT	2280
20	AGTTTCAAAA TATTGTGGTT TAGTAAAGTT GATACCTGGT TATAAATATT ATGCCTTTAT	2340
	TTTTGGCTAG AAGAAGAAIT ATTTTTAGCC TAGATCTAAC CATTTTCATA CTCTTAACTG	2400
25	ATTGAAACAG ATTCAAAGAA GTATCGAGTG CTATGCATTG AAACCTGTTT TTAAATGTTA	2460
	GATGGCACTA TGTATATTAA TGTAACAA TGTTAATTTA CTCAAGTTTT CAGTTTGTAC	2520
	CGCCTGGTAT GTCTGTGTAA GAAGCCAATT TTTGTGTATT GTTACAGTTT CAGGTTATTT	2580
30	ATATTGATG TTTTGTAAAA CTCAAATAAC GACTATACTT ATGGACCAAA TAAATGGCAY	2640
	TGCATTCTKG TKAAAAAAN NACAGAAAAA AAAAAAACA AGA	2683
35		

(2) INFORMATION FOR SEQ ID NO: 295:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

	GGACTCGGGG TGGCTCTAAG GGGCAGGGAT AGGGCTGGGG AGCGCCGGCC TGTGGCCCTG	60
50	ACCAGCCCCC TCTCGTGCAG GTTCCACCCC GATGCAGGTG GTCACGTGCT TGACGCGGGA	120
	CAGCTACCTG ACGCACTGCT TCCTCCAGCA CCTCATGGTC GTGCTGTCTT CTCTGGAACG	180
	CACGCCCTCG CCGGAGCCTG TTGACAAGGA CTTCTACTCC GAGTTTGGGA ACAAGACCAC	240
55	AGGGAAGATG GAGAACTACG AGCTGATCCA CTCTAGTCGC GTCAAGTTTA CCTACCCAG	300
	TGAGGAGGAG ATTGGGGACC TGACGTTTAC TGTGGCCCAA AAGATGGCTG AGCCAGAGAA	360
60	GGCCCCAGCC CTCAGCATCC TGCTGTACGT GCAGGCCTTC CAGGTGGGCA TGCCACCCCC	420

TGGGTGCTGC AGGGGCCCCC TGCGCCCCAA GACACTCCTG CTCACCAGCT CCGAGATCTT 480
 CCTCCTGGAT GAGGACTGTG TCCACTACCC ACTGCCCCGAG TTTGCCAAAG AGCCGCCGCA 540
 5 GAGAGACAGG TACCGGCTGG ACGATGGCCG CCGCGTCCGG GACCTGGACC GAGTGCTCAT 600
 GGGCTACCAG ACCTACCCGC AGCCCTCACC CTCGTYTTCG ATGACGTGCA AGGTCATGAC 660
 10 CTCATGGGCA GTGTCACCCT GGACCACTTT GGGGAGGTGC CAGGTGGCCC GGCTAGAGCC 720
 AGCCAGGGCC GTGAAGTCCA GTGGCAGGTG TTTGTCCCCA GTGCTGAGAG CAGAGAGAAG 780
 CTCATCTCGC TGTGTGGCTG CCAGTGGGAG GCCCTGTGTG GCCTGAGCTG CCTGTGAGC 840
 15 TCACCGGCTA GCCCAGGCCA CAGCCAGCCT GTCGTGTCCA GCCTGACGCC TACTGGGGCA 900
 GGGCAGCAGG CTTTGTGTGT CTCTAAAAAT GTTTTATCCT CCCTTTGGTA CCTTAATTTG 960
 20 ACTGTCTCG CAGAAATGTG AACATGTGTG TGTGTGTGT TAATTCCTTC TCATGTTGGG 1020
 AGTGAGAAATG CCGGGCCCCCT CAGGGCTGTT CGGTGTGCTG TCAGCCTCCC ACAGGTGGTA 1080
 CAGCCGTGCA CACCAGTGTG GTGTCTGCTG TTGTGGGACC GTTGTAAACA CGTGACACTG 1140
 25 TGGGTCTGAC TTTTCTTCT ACACGTCTTT TCCTGAAGTG TCGAGTCCAG TCCTTTGTTG 1200
 CTGTTGCTGT TGCTGTGCT GTTGCTGTG GCATCTTGCT GCTAATCCTG AGGCTGGTAG 1260
 30 CAGAATGCAC ATTGGAAGCT CCCACCCCAT ATTGTCTTTC AAAGTGAGG TCTCCCTGA 1320
 TCCAGACAAG TGGGAGAGCC CGTGGGGGCA GGGGACCTGG AGCTGCCAGC ACCAAGCGTG 1380
 ATTCCTGCTG CCTGTATTCT CTATTCCAAT AAAGCAGAGT TTGACACCGW MAAAAAAAAA 1440
 35 AAAAAAAAAA AACN 1454

40

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

55

ACCCTGGCAT GCCCCACAAA CAGATCACCA GCCAGCTTAC ACAGGCATTA ACTCTCCTCA 60
 ATGAGGAAGA ATCATTCACA ACTGAGCAAG ACATTCATAT GATCATTTAA GGAAGTGTMT 120
 CCCTTATGTG TTAGCAAGTA TAATCGGCTA ACTCCTAAAT CCCAATGAAT AGTCCTAGGC 180
 TGGACAGCAA TGGGCTGCAA TTAGGCAGAT AAAGACATCA GTCCAGTAA ATGAATCCAT 240
 60 AGACTCATCT AGCACCAACT ACCATTAGCA CTATGTTAGG AGCTGCAAGG CCCCAGTA 300

GAAGATGTGC ATAATGTCTG CTCTTGTTA GTCAGGAGA CAATTCAGC ACAGACACTA 360
CAGTTAACGC TGAAGTCAG CTGCAAGTAA TAGCAWGAAC AGTCAGAAAA ATACCTTATG 420
5 AGGGGGCAGG GCTGAAGCTG GGCCTGAAG GATGGATGAA ATMTGGATAG AGAATGAGGA 480
AGACAGAGGG NCTCCAAGTG AGAGAAGCAT GAAAAATGAG CARGGGCCTG GATCAGTGGG 540
GTGTATTTCAG AGCACCCTTC CAGATGCACC ATGCATGCTC ACAGTCCCTT GCCTATGTGT 600
10 GGCAGAGTGT CCCAGCCAGA TGTGTGCCCC CACCCCATGT CCAATTACAT GTCCTTCAAT 660
GCCACCTCA AAAGGYACYT CTTCTGTAAA GCTTTCCCTK GGTATCAGGA ATCAAAATTA 720
15 ATCAGGGATC TTTTCACACT GCTGTTTTT CTTCTTTGGT CCTTCTATCA CTAAAACTCA 780
TCTCATTCAG CCTTACAGCA TAACTAATTA TTTGTTTTCC TCACTACA 828

20

(2) INFORMATION FOR SEQ ID NO: 297:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2416 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

35

TCAATTTCCA TTAAGTCAGA TCAGCCATTG TGATTCACCA TTTGTCAGGC TCTCAGGTTT 60
AACAAAACCT ACTATCACCA TCATCCTTCA ACAGCCACAG TCTGAATTGA GCCAACATTT 120
TTTTTTCTTT GAGAAAGAAG TGGACTGGGG CACAACTTTT AGTCTGAGGG GAGCTAGTGG 180
AAATCTAGAC AATAGAAGTC ATCGATAGCA GCTTTTCCTC AAATGTGTGA CTCCTCAGGG 240
40 GCTAAACTGC TCTTAGCTTA GAATTATGCT TTAGTAGAGA TCTAGCAGAT AAGTGGGTTA 300
ATCACTACCA TCCTGTAACT AGTTATATAG CTTCACAGCA TGAGGGAGAC ATCAAAACAGG 360
GATGGAAGCA ACCCAAGGA TATGCAAGAA GGGCATGATG AACCCCTTC CCTCTGGCAG 420
45 GAGAACAAGG CCAACCAAGG GACAGACTGG AAAGCACTTA GATGTTTAAG GAGGAGAAAG 480
GGGAAGCTTT GACCAGTCTT TGCTTTTTC CAAGTTCAGC CAGTTCTCCG CTGCTTGCAA 540
CCTCTAGCGC AGTAACATTT GCAGAATTGC AGATTTTCCC CCAGATACTA GGAGGAAAGG 600
GACTTTGGGG GGTGGGAAG GGTGCTGGT GTTTTAAAAG CATAAGTTAC CTGTTTGAC 660
50 TGTTTTAAGA TAGGAAAAA AAATAGTGGG CAAGGTGAAC ATCAGACGTA AATTTGTGTG 720
TTTTTATTTT GTCATGCTCT TGAAATGTT TGACCATTTG TAGTATACAC AGTGAACTT 780
GATTCTCTGT TGCATAAAC ACTATATTTT TTTGAAATG TTAGTGTCCA AAAGCCTCTT 840
60 CCTTCCCTTT CCTTTTCTTA TGTACTTCCT TCATACTTGC TTTACTGATC AGCCAGGCAA 900

5 TAGCCATCCA AGAGCTAGAG CATGAAACAG GGCCTTTCC AAGTAGGCTC TGGGTGTCCT 960
AAGCCAGCGT GTGCCCTCTG GTTTAGTGAG TGTAAATAGAG TCCCTGGCAC CTTTCTTTGC 1020
AAATGAGGCT AACAGACCAG ACTGCAGCAA GTTATCAGAT TCCTCAATCA GATGCACTAG 1080
GAGTGAGGAG CCCAGGGATG GAGGGGGTTC CTGAAGTATT GCAGTTGGCT GTAGTAGCTG 1140
10 AGTTCTTTTC CATGTTACCG AACTGTAGC CAGTTACAGT TTAICTAGGA AAACGGTAGA 1200
TCAATTCAGC CATGGTAGTG CTGGTTGGCA GGGATTGGTA ACGGAGAGAA CTGCTCATCA 1260
GCCAAACTC AAGCCTTGCC TTTTAGGAGG CCACCAGCAG AGGGACTTGG TCCTCCTTGT 1320
15 CTGGTACTTG TGTACATGCC GGTGACCTGA GGACTCCACT CACACTGGCG AGCAAAAAGG 1380
GAGCAGTGAT TCTCTTTTCT CTCCCCACCC CCTGCCCTTT GTTACCAACA CCAGTTTCCC 1440
20 AGGGGTACA TGAGTTTCTG AATTTTAAA AAATGTTTTT GGTGTTGTTT TTCTGGGGAC 1500
TGATAAGTGC TTAAAGCAAT GTCCATACCC CGTCAAGACT CCCAGCTTAG TCATTTTCTT 1560
GTATTTTCT GTTCACAGTA TTTGTGTGTG TGCTTGTTTT GGCAGCTCAT TTTGGCTGTA 1620
25 TTATATATTG AGTGATGAAT TGATCCTCTT TTTTCCCTAA GGGATATGAA TTGTTTTTCT 1680
TGTGTTATAT TCTGCTGTG AATAGCTGGA GCAAACCTGG GGCTGACAG CGTAAGSTAG 1740
30 GGCTGCAAAAR CGAGAAGAGA GCCGGTGGAG TGTACTTGTG CCTGACAGG TGACCTACCT 1800
GAGTCTCTGA GCTTTTCAGT CCAATCTTT GCAAGGCTCA AAATGCCACA GAACCTCTCC 1860
TCTTCTCCCC ACTCCCCATG GCAGGGACCG GACCATCCCT ACATGCAACA TGCTGTTCTT 1920
35 CCAGCCCCCTC CCATTGCCAT GGCAAAACAG GTACCTTTGG GGCATGGGG CATTACATGG 1980
GATGCTTG TG TAATCGACCA CTTAGCCTTC TCTCTCCCCT CCGTCTCTCC CCCAGAATCA 2040
40 CTTCCTAGGA CACCCGAGCT GCTTGCCAG GGTCTGTTTT CCCTGCTAAC TCCAGAGAAG 2100
CATCCAGGG CTTGTGACA GTCTCTAATT CCCTTCCCTT CTCGTTAAGA ATCATATTGT 2160
ATAGTAGCTT TCAGACCATA CAGTATTCAT TGGGTACTC CTATTATTAT CAAGTAGCTG 2220
45 GAATTGTGAA GGTGGAGTA GTTAGATCTT TAGCTTTTAT TCCTTATTTT TTTGTATTAC 2280
TCTCCATGTG TATAAATTAT TGATCATGTT GCTGGCTTTT ATAAACTCTA AGCGAAGGAG 2340
50 GAGCACTGCC TCAGCCTTTG CACATGGTAA TGAAGCACTG TTTTAAATA AAAGRGRGAA 2400
MCMCCAAAA AAAAAA 2416

55

(2) INFORMATION FOR SEQ ID NO: 298:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 base pairs

60

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GAATTCGGCA CGAGCCATGC YTGCCCTCTC CTTGATTCTT ACAGTCACTT TGTGCGCTGT 60
TTCTGACTCA GCAGCTACCT GCATTGTGGC CAAAGGATGA CCTATTCTTT CTCAGGAGGG 120
10 CAAAAATGTG GAATAGTGTC TGTCCATGCC TCTCCTCATG GGCTACCACC TCTGCCACCG 180
TGGTTAATCA GTAACAACCA GGAGAGAAGC TGCTGGAAC TACCTCTGGG AACTCCCTGG 240
15 ATGGTTTGGT GCAGGAATGT AGTAGGCATA CACGTGGTTG CGTGGATCTG GGCCCTCCTG 300
ATGTGAGTAG AGAGGTAAAA GGSCACCATC TCCTTGACCT YTGCGGAACT CATCCACAAA 360
GAAGATGTTT CCAAGATGCT TCTGAAGATT GSCTAAAAAT AGCCGGTTTC CACCCCGTG 420
20 AATGCATCCA TTCTAGAATG CTCCTTCACC AGGACCAGAG AACTGATTTA CAGAAGTGAC 480
ATGAAAACAT TCCATCCCAG AATTTGCANT ACCTCAAATT NAATTTCTAC CTATTAAAAA 540
25 NAAAA 545

30 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1530 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

40 GGCTCTGCTG GGCATCATAC TTGTCACTGG GTAAACAGTT TGCCCACTTA CCGCAGATGA 60
AGCTGCTTGC CAGGGCTCTC CGGCTCTGTG AGTTTGGGAG GCAGGCATCT TCCAGGAGGC 120
TGGTGGCTGG CCAGGGATGT GTGGGGCCCC GCGAGGGTG CTGCGCTCCC GTCCAGGTGG 180
45 TTGGGCCAG GGCTGATCTC CCACCTGTG GAGCTGCAT TACTGGAAGG ATCATGCGGC 240
CAGATGATGC CAACGTGGCC GGCAATGTCC ACGGGGGGAC CATCTGAAG ATGATCGAGG 300
50 AGGCAGGCGC CATCATCAGC ACCCGGCATT GCAACAGCCA GAACGGGGAG CGCTGTGTGG 360
CGCCCTGGC TCGTGTGAG CGCACCAGCT TCCTGTCTCC CATGTGCATC GGTGAGGTGG 420
CGCATGTGAG CGCGGAGATC ACCTACACCT CCAAGCACTC TGTGGAGGTG CAGGTCAACG 480
55 TGATGTCCGA AAACATCTTC ACAGGTGCCA AAAAGCTGAC CAATAAGGCC ACCCTGTGGT 540
ATGTGCCCTT GTCGCTGAAG AATGTGGACA AGGTCTCTGA GGTGCTCTCT GTGTGTATT 600
60 CCCGGCANGA GCAGGAGGAG GAGGGCCGGA AGCGGTATGA AGCCGAGAAG CTGGAGCGCA 660

5 TGGAGACCAA GTGGAGGAAC GGGGACATCG TCCAGCCAGT CCTCAACCCA GAGCCGAACA 720
CTGTACAGCTA CAGCCAGTCC AGCTTGATCC ACCTGGTGGG GCCTTCAGAC TGCACCTGCG 780
ACGGCTTTGT GCACGGAGGT GTGACCATGA AGCTCATGGA TGAGGTCGCC GGGATCGTGG 840
10 CTGCACGCCA CTGCAAGACC AACATCGTCA CAGCTTCCGT GGACGCCATT AATTTTCATG 900
ACAAGATCAG AAAAGGCTGC GTCATCACCA TCTCGGGACG CATGACCTTC ACGAGCAATA 960
AGTCCATGGA GATCGAGGTG TTGGTGGACG CCGACCCTGT TGTGGACAGC TCTCAGAAGC 1020
15 GCTACCGGGC CGCCAGTGGC TTCTTCACCT ACGTGTGCT GAGCCAGGAA GGCAGGTCCG 1080
TGCTGTGCC CCAGCTGGT CCCGAGACCG AGGACGAGAA GAAGCGCTTT GAGGAAGGCA 1140
AAGGGCGGTA CCTGCAGATG AAGCGAAGC GACAGGGCCA CGCGAGCCT CAGCCCTAGA 1200
20 CTCCTCTCTC CTGCCACTGG TGCTTCGAGT AGCCATGGCA ACGGGCCAG TGTCCAGTCA 1260
CTTAGAAGTT CCCCCCTGG CCAAAAACCC AATTCACATT GAGAGCTGGT GTGTCTGAA 1320
GTTTTCTGAT CACAGTGTTA ACCTGTACTC TCTCTGCAA ACCTACAC CAAAGCTTTA 1380
25 TTTATATCAT TCCAGTATCA ATGCTACACA GTGTGTCCC GAGGCGCGG AGGCGTTGGG 1440
CAGAAACCT CGGAATGCT TCCGAGCAG CTGTAGGTA TGGGAAGAAC CCAGCACCA 1500
30 TMATAAGCT GNTGCTTGGC TGGGAAGNA 1530

35 (2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 997 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

45 AGGTAGTGAG AGACACATTA CACCTAACCA ACAAGAAGAA GGATCCTCCC CCTTATAATT 60
TAACTATGTT TACAGGGAAT GCGTACATTG TGGCTTCCCG AGNATTTCTG CCAACATGTT 120
TTGAAGAACC CTAATCCCA ACAACTGATT GAATGGGTAA AAGACACTTA TAGCCCAGAT 180
50 GAACACCTCT GGGCCACCCT TCAGCGTGCA CGGTGGATGC CTGGCTCTGT TCCCAACCAC 240
CCCAAGTACG ACATCTTCAG ACATGACTTC TATTGCCAGG CTGGTCAAGT GGCAGGTCA 300
55 TGAGGGAGAC ATCGATAAGG GTGCTCCTTA TGCTCCCTGC TCTGGAATCC ACCAGCGGC 360
TATCTGCGTT TATGGGCTG GGGACTTGAA TTGGATGCTT CAAACCATC ACCTGTTGGC 420
60 CAACAAGTTT GACCCAAAGG TAGATGATAA TGCTCTTCAG TGCTTAGAAG AATACCTACG 480

TTATAAGGCC ATCTATGGGA CTGAACCTTG AGACACACTA TGAGAGCGTT GCTACCTGTG 540
 GGGCAAGAGC ATGTACAAAC ATGCTCAGAA CTGCTGGGA CAGTGTGGGT GGGAGACCAG 600
 5 GGCTTTGCAA TTCGTGGCAT CCTTTAGGAT AAGAGGGCTG MTATTAGATT GTGGTAAGT 660
 AGATCTTTTG CCTTGCAAAT TGCTGCCTGG GTGRATGCTG CTTGTTCTCT CACCCCTAAC 720
 CCTAGTAGTT CCTCCACTAA CTTTCTCACT AAGTGAAT GAGAACTGCT GTGATAGGGA 780
 10 GAGTGAAGGA GGGATATGTG GTAGAGCACT TGATTTCACT TGAATGCCTG CTGGTAGCTT 840
 TTCCATTCTG TGGAGCTGCC GTTCCTAATA ATTCCAGGTT TGGTAGCGTG GAGGAGAACT 900
 15 TTGATGGAAA GAGAACCTTC CCTTCTGTAC TGTAACTTA AAAATAAATA GCTCCTGATT 960
 CAAAGTAAGG AAAAARAAAA AAAGAAAAA AACTCGA 997

20

(2) INFORMATION FOR SEQ ID NO: 301:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

TTGAGGCCGA CGCTAGGGGC CCGGAAGRAA ACTGCGAGGC GAAGGTGACC GGGGACCGAG 60
 CATTTCAGAT CTGCTCGGTA GACCTGGTGC ACCACCACCA TGTGGCTGC AAGGCTGGTG 120
 35 TGTCTCCGA CACTACCTTC TAGGGTTTTC CACCAGCTT TCACCAAGGC CTCCCCTGTT 180
 GTGAAGAATT CCATCAGAA GAATCAATGG CTGTTAACAC CTAGCAGGGA ATATGCCACC 240
 40 AAAACAAGAA TTGGGATCCG GCGTGGGAGA ACTGGCCAAG AACTCAAAGA GGCAGCATTG 300
 GAACCATCGA TGGAAAAAAT ATTTAAATTT GATCAGATGG GAAGATGGTT TGTGCTGGA 360
 GGGGCTGCTG TTGGTCTTGG AGCATGTGC TACTATGGCT TGGGACTGTC TAATGAGATT 420
 45 GGAGCTATTG AAAAGGCTGT AATTTGGCCT CAGTATGTCA AGGATAGAAT TCATTCCACC 480
 TATATGTACT TAGCAGGGAG TATTGGTTTA ACAGCTTTGT CTGCCATAGC AATCAGCAGA 540
 50 ACGCCTGTTT TCATGAACCT CATGATGAGA GGCTCTTGGG TGACAATTGG TGTGACCTTT 600
 GCAGCCATGG TTGGAGCTGG AATGCTGGTA CGATCAATAC CATATGACCA GAGCCCAGGC 660
 CCAAAGCATC TTGCTTGGTT GCTACATTCT GGTGTGATGG GTGCAGTGGT GGCTCCTCTG 720
 55 ACAATATTAG GGGGTCTCT TCTCATCAGA GCTGCATGGT ACACAGCTGG CATGTGGGA 780
 GGCTCTCCA CTGTGCCAT GTGTGCGCCC AGTGAAGT TTCTGAACAT GGGTGCACCC 840
 60 CTGGGAGTGG GCCTGGGTCT CGTCTTTGTG TCCTCATTGG GATCTATGTT TCTTCCACCT 900

	ACCACCGTGG CTGGTGCCAC TCTTTACTCA GTGGCAATGT ACGGTGGATT AGTTCTTTTC	960
	AGCATGTTCC TTCTGTATGA TACCCAGAAA GTAATCAAGC GTGCAGAAAT ATCACCAATG	1020
5	TATGGAGTTC AAAAATATGA TCCCATTAAC TCGATGCTGA GTATCTACAT GGATACATTA	1080
	AATATATTTA TCGGAGTTGC AACTATGCTG GCAACTGGAG GCAACAGAAA GAAATGAAGT	1140
10	GACTCAGCTT CTGGCTTCTC TGCTACATCA AATATCTTGT TTAATGGGGC AGATATGCAT	1200
	TAAATAGTTT GTACAAGCAG CTTTCGTTGA AGTTTAGAAG ATAAGAAACA TGTCAATATA	1260
	TTTAAATGTT CCGGTAATGT GATGCCTCAG GTCTGCCTTT TTTTCTGGAG AATAAATGCA	1320
15	GTAATCCTCT CCCAATAAG CACACACATT TTCAATTCTC ATGTTTGAGT GATTTTAAAA	1380
	TGTTTTGGTG AATGTGAAAA CTAAAGTTTG TGTCAAGAGA ATGTAAGTCT TTTTCTACT	1440
20	TTAAAATTTA GTAGGTTTAC TGAGTAACTA AAATTTAGCA AACCTGTGTT TGCATATTTT	1500
	TTTGGAGTGC AGAATATGT AATTAATGTC ATAAGTGATT TGGAGCTTTG GTAAAGGGAC	1560
	CAGAGAGAAG GAGTCACCTG CAGTCTTTTG TTTTTTTAAA TACTTAGAAC TTAGCACTTG	1620
25	TGTTATTGAT TAGTGAGGAG CCAGTAAGAA ACATCTGGGT ATTTGGAAAC AAGTGGTCAT	1680
	TGTTACATTC ATCTGCTGAA CTTAACAAAA CTGTTTCATCC TGAAACAGGC ACAGGTGATG	1740
30	CATTCTCCTG CTGTTGCTTC TCAGTGCTCT CTTTCCAATA TAGATGTGGT CATGTTTGAC	1800
	TTGTACAGAA TGTTAATCAT ACAGAGAATC CTTGATGGAA TTATATATGT GTGTTTACT	1860
	TTTGAATGTT ACAAAGGAA ATAACTTTAA AACTATTCTC AAGAGAAAAT ATTCAAAGCA	1920
35	TGAAATATGT TGCTTTTCC AGAATACAAA CAGTATACTC ATGATTGCTA AGTGTMTTTT	1980
	TATTTTGTCA TATTTATTGA ACTGTCTAAT TGAATACAGC TTGCTCTTGT CACCTCTTCA	2040
40	AGCTTTCAAG CCTTTATAGA AAAGCTTCTT TGTGGCTTAC ACTGGAAATT ATGAAAGCAG	2100
	TTTTTCTCCT AAGACTTTTG GTTTCTCGCA TTGCCTCTCA GACTAAGCAC TAAAAAGCAA	2160
	AGCAAAACAG AACTAGTNCT GTCTTAATGA AATATATCAA CCCAAAAGTG TAATGAGGAA	2220
45	AATGCTTCAT TAGTTTCCCC TAGCAGACTT TTACTTCTCT TACACTGCTA CACCATTACT	2280
	TTCTTGAGAC ATTTGTAAGT CCTTTGATAC AGAAGAGTTA TATTTAGGAG GNCTTTAATG	2340
50	AAGGG	2345

55 (2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

5	TTTTTTTTTT TTTTTTTTTT TTTTINCAAG ATCATTTGTTT ATTTATTACT TCAGATAAAA	60
	AGATAGTATA CATATTAGGG AATCCCTTAA AATTCAACTC TAGAGTTATA CACCATCTAG	120
	TACTTTTGCA ATGAATGTTA ACAACAACAA AAAAAATCTC TAAACACCTG AAAGCCCCAC	180
10	TATTAACATG GACTATGGTA ATAAAAAATT TTGACATTTA ATTTGTTCAA CATATAGTAT	240
	TTACATTATG AAACCAATGG TGATGATACA ATAAAGTGAT AAAGAAATAG TAAAAATAAA	300
15	CTTTAAAAAG CAAAGGTTTA TAGTCTGACA ATGCTAATTA TCCTAATTGT ATATAAAAAA	360
	TTAAACATA GAGCTTTCTG TTACAAAATT CTTAATCCTC TGGGTTGTAA TCATTACTTG	420
	CTACCAATTT ACATGCAACA TCTGCTAGGA CTGACATTTG ATTTTTTTTCC CCAAGAATGT	480
20	GTGAGTAGAT AAATGACATT TCAGAGCAGA TATTAATTTA CTTGTGGACA GAAAAAGAAA	540
	CTCAAGATTG GTACTGGTCA CAAGCCTCTT CCCAATAGAA ATTATAAAAA CAGTAAGATA	600
25	AAATTTAAAA AAAATCTAAA AAGGGGATGC ATAGGCAAAG AGTACCATAA ATGGCACAGC	660
	TCAAAAAATC CCAGGACCAA TCAGACACAC ATCTTTTCTC TCTCCTTCAG CGACAAGAGG	720
	TCGATTTTGC CATCAAATAA CCATGATTGA AGCAAGCGAG GGGCACCAGG TGTACAACTG	780
30	ATTAGATCTT GCAAATACT AAGATGGGAG CAGGGGTGGC CAGAAGAAGG GGTAAATTTAT	840
	ATATAATTCA AACTATATAC AGCATAAATG GAATGCAGCC CATCCCAAAC TGGCTCTGIG	900
35	AAACAATTGG ACCTTTATAG TTAAAATTAT AACAAGTGTA ATAATACAAT AGATTTACAT	960
	GGGAAGCAAA ATCCAAGGGA CATTTTATAT TAAGTATTTA CTGTGCTGTT TCAATTTAAA	1020
	AATAATTTTG CTAAGTATAC ATCTCAACTG AAGTCTATGT AAAAAATGTC CTAATAGATA	1080
40	CAGATATTTA CCTTTGGTGA GTTGAAGGCC TTTTGTGAC TTCTGTCTGA ACTGTAGGCA	1140
	GAATGCTAGA TGTACATGCA CATATGGAGA AACTCAAGCT GAGGTCATCC AAAAGCTGTG	1200
45	CGTATGAGGA GGCTGGAGGT ACTTTGAAAG TCAAAGTAGA CCAGAAACCC AAAACAGGTA	1260
	ACAGTGAGGA TGGCAACAGG GAATGGAATG CCAATATGGC AGTAAACTT TTTTTAAAAA	1320
	CAGAAAGAGG AAGGCTCTC GTACCAGCAG AATCCTGTAC ACGTACAAAA AAGAAAAAGC	1380
50	CACCCACCAT TTTGTAAAAC AGAAGCCAAT TATAGTGTGG GAAAGTACAA ATTACAGAAA	1440
	ACCAGAAGTC AACAGAAGAA AACTACTTGG TTTACTTGAG AGAAAGGAGA ATGGTTCACC	1500
55	CCGAGCAGAG TTACTTGGTG AACGCCGCCA CCACCGCCCA CAGAACCTCA TTGGTGTGG	1560
	CCTTCAGACA TTCCACTTCA GGGTCTAAGT CGAGAARNVG CCGCACTCTC TTGGTAGCCA	1620
60	AATCATACTG CTCGTCCAGA AGAGGAGCAA AAGCATTTCT CAGGACGTCC GAGGCATGAG	1680

CCAGGTAAAT GAGGGCCAGC AAGCGCCTGT CCATGCCGTG AGGGTCATTC ACCCATTTGT 1740
CAAGAACGGC TTCCTGTACT TTCTTGATGA GCGCCTGCTT AATGTTGTTA TTGGTGAGGG 1800
5 GATGTGTTGT CATGTCAAAA AGTAGGAAGT TCTGTTTCTC TGTGTCAAT ACACCCCTTTT 1860
CCACCAGGTT TTAGCTAAT CGTTCCCGTA CATTTCTTAA CTGATAATGC AATTTTAATG 1920
10 GATTCCATGT CTCACCACTA AGTAATTCAA TCCAGTTCTG GACCGTTTCT GGAGGCTGAG 1980
TTTCCTTAAC ATGCTTCAGA GCTTCATCAA GAAGAACATC CCCTGTTGGA GCATCTGACT 2040
TACAGATTAC CTTTCTTGTT AATAGACTTT TACGTCTCAT TCCACAAGCC TCTAGTTGTA 2100
15 ACCTTCCTCT CAATGCTAAT TCAATTAACA TACAGCCACG TAATCCAGAT GATATACAGT 2160
CATTCACAAA TGATGTGTAA ACCTTCGCGG TCCTTGAGGC CCAGCAGGAG CACTTCCTCC 2220
ATCAGGGTCA CCCGCGTTTC CTTGGAGTCG CCCTTGTCGT CGTCGTCTG CTCGTGCGG 2280
20 CGGCTCTGCG CGTCGTCTC GCTGCTAGCC GCGCCGCGC CCGCCGCCG CTCCTTGTCG 2340
GCGGCGTTGC GGGAGGCCTC GGTGCGCCG 2369
25

(2) INFORMATION FOR SEQ ID NO: 303:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GGGACGTGTG GTTTCAGCTC GTGCGCCTCC CCGTGGGTTT GCGACGTTTA GCGACTATTG 60
40 CGCCTGCGCC ACGCCGGCTG CGAGACTGGG GCCGTGGYTG CTGGTCCCGG GTGATGCTAG 120
GCGGCTCCCT GGGCTCCAGG CTGTTGCGGG GTGTAGGTGG GAGTCACGGA CGGTTCCGGG 180
45 CCGAGGTGT CCGCGAAGGT GGCGCACATG GGCGGCAGGG GAGAGCATGG CTCAGCGGAT 240
GGTCTGGGTG GACCTGGAGA TGACAGGATT GGACATTGAG AAGGACCAGA TTATTGAGAT 300
GGCCTGTCTG ATAAGTACT CTGATCTCAA CATTTTGGCT GAAGGTCCTA ACCTGATTAT 360
50 AAAACAACCA GATGAGTTGC TGGACAGCAT GTCAGATTGG TGTAAAGGAGC ATCACGGGAA 420
GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG TACAATTACA TTGCAGCAGG CAGAGTATGA 480
ATTTCTGTCC TTTGTACGAC AGCAGACTCC TCCAGGGCTC TGTCCACTTG CAGGAAATTC 540
55 AGTTTCATGAA GATAAGAAGT TTCTTGACAA ATACATGCCC CAGTTCATGA AACATCTTCA 600
TTATAGAATA ATTGATGTGA GCACTGTAA AGAACTGTGC AGACGCTGGT ATCCAGAAGA 660
60 ATATGAATTT GCACCAAAGA AGGCTGCTTC TCATAGGGCA CTTGATGACA TTAGTGAAAG 720

CATCAAAGAG CTTCAAGTTT ACCGAAATAA CATCTTCAAG AAAAAAATAG ATGAAAAGAA 780
 5 GAGGAAAATT ATAGAAAATG GGGAAAATGA GAAGACCGTG AGTTGATGCC AGTTATCATG 840
 CTGCCACTAC ATCGTTATCT GGAGGCAACT TCTGGTGGTT TTTTTCCTC ACGCTGATGG 900
 CTTGGCAGAG CMCTTCGGTT AACTTGCATC TCCAGATTGA TTAACAAGC AGACAGCACA 960
 10 CGAAATACTA TTTTCTCCT AATATGCTGT TTCCATTATG ACACAGCAGC TCCTTTGTAA 1020
 GTACCAGGTC ATGTCATCC CTTGGTACAT ATATGCATTT GCTTTTAAAC CATTTCTTTT 1080
 GTTTAAATAA ATAAATAAGT AAATAAGCT AGTTCTATTG AAATGCAAAA AAAAAAAAAA 1140
 15 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA N 1181

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(2) INFORMATION FOR SEQ ID NO: 304:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1537 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

CTTTGTGT TCCGGCGAT CCCACCTCTC CTCGACCTG GACGTCTACC TTCCGGAGGC 60
 CCACATCTG CCCACTCCGC GCGCGGGGCT AGCGCGGGT TCAGCGACGG GAGCCCTCAA 120
 35 GGGACATGGC AACTACAGCG GCGCCGCGG GCGGCCCGG AANATGGAGC TGGCCCGGAA 180
 TGGGAGGGT TCGAAGAAAA CATCCAGGGC GGAGGCTCAG CTGTGATTGA CATGGAGAAC 240
 40 ATGGATGATA CCTCAGGCTC TAGCTTCGAG GATATGGGTG AGCTGCATCA GCGCCTGCGC 300
 GAGGAAGAAG TAGACGCTGA TGCAGCTGAT GCAGCTGCTG CTGAAGAGGA GGATGGAGAG 360
 TTCCTGGGCA TGAAGGGCTT TAAGGGACAG CTGAGCCGGC AGGTGGCAGA TCAGATGTGG 420
 45 CAGGCTGGGA AAAGACAAGC CTCCAGGGCC TTCAGCTTGT ACGCCAACAT CGACATCCTC 480
 AGACCCTACT TTGATGTGGA GCCTGCTCAG GTGCGAACAG GGCTCCTGGA GTCCATGATC 540
 CCTATCAAGA TGGTCAACTT CCCCCAGAAA ATTGCAGGTG AACTCTATGG ACCTCTCATG 600
 50 CTGGTCTTCA CTCTGGTTGC TATCCTACTC CATGGGATGA AGACGTCTGA CACTATTATC 660
 CGGGAGGGCA CCCTGATGGG CACAGCCATT GGCACCTGCT TCGGCTACTG GCTGGGAGTC 720
 55 TCATCCTTCA TTTACTTCCT TGCCTACCTG TGCAACGCCC AGATCACCAT GCTGCAGATG 780
 TTGGCACTGC TGGGCTATGG CCTCTTTGGG CATGCAATG TCCTGTTCAT CACCTATAAT 840
 60 ATCCACCTCC ACGCCCTCTT CTACCTCTTC TGGCTGTTGG TGGGTGGACT GTCCACACTG 900

CGCATGGTAG CAGTGTGGT GTCTCGGACC GTGGGCCCCA CACAGCGGCT GCTCCTCTGT 960
 GGCACCTGG CTGCCCTACA CATGCTCTTC CTGCTCTATC TGCAITTTGC CTACCACAAA 1020
 5 GTGNTAGAGG GGATCCTGGA CACACTGGAG GGCCCCAACA TCCCGCCCAT CCAGAGGGTC 1080
 CCCAGAGACA TCCCTGCCAT GCTCCCTGCT GCTCGGCTTC CCACCACCGT CCTCAAAGCC 1140
 10 ACAGCCAAAG CTGTTGCGGT GACCCCTGCAG TCACACTGAC CCCACCTGAA ATTCTTGCC 1200
 AGTCTCTTT CCCGCAGCTG CAGAGAGGAG GAAGACTATT AAAGGACAGT CCTGATGACA 1260
 TGTTCGTAG ATGGGGTTG CAGCTGCCAC TGAGCTGTAG CTGCGTAAGT ACCTCCTTGN 1320
 15 AGCTGTCGGC ACTTCTGAAA GCACAAGGCC AAGAACTCCT GGCCAGGACT GCAAGGCTCT 1380
 GCAGCCAATG CAGAAAATGG GTCAGCTCCT TTGAGAACCC CTCCCCACCT ACCCCTTCCT 1440
 TCCTCTTTAT CTCTCCACA TTGTCTTGCT AAATATAGAC TTGGTAATTA AAAAAAAAAA 1500
 20 AAAAAAAAAA AAAAAAAAAA AAAAAAGGG GGNCCCC 1537

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(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

TGCATGCCAA AACCAATGCC TGCCAAACAA AATCTTAGAC ATCCCAATAT AATATGTTAG 60
 TTATATTTCT ATTACATCA TTATTGAAAA TACCCAGCTC AGTGCCTGGC TTAATAAATG 120
 40 TTTAATTCCC TTACCTACTC TTGCTCTATT TTTTATTG AAATGGAGAT GAGCAAAATA 180
 ACACATTCAT GGCTGAAGCA ATTTTTTGGA CATTTCTTGT TACCAAAAGA TCTATAATCA 240
 45 GGATGATCCT GAGCTGTTCA AACAAAGCTGT ATATAACAG ACAATGAAAC TCTTTGCAGA 300
 GCTGGAAATT AAAAGGAAAG AGAGAGAAGC CAAAGAGATG CATGAAAGGA AACGACAAAG 360
 GGAAGAAGAG ATTGAAGCTC AAGAAAAAGC CAAACGGGAA AGAGAGTGGC AGAAAACTT 420
 50 TGAGGAAAGT CGAGATGGTC GTGTGGACAG CTGGCGAAAC TTCCAAGCCA ATACGAAGGG 480
 GAAGAAAGAG AAGAAAAATC GGACCTTCCT GAGACCACCG AAAGTAAAAA TGGAGCAACG 540
 TGAGTGACCG CCCAAGGTCA CAGGCACAGA ACCTTTCCCC TGCTATCTCC CTTCTGCTT 600
 55 CGAAGGACTC ATTCTTTCCT CCCACTTCCA CCCCAACATA GAGTAGTATT TGCTTTTATG 660
 TCCATTTTGT TTTCAATACG ATTTAATATC GATCAGAGTA ATTCTTTTGT ACATTGAAAT 720
 60 GAGGGGCTTG GTTTAAAAA AGACCTTTCC CTCTCCCTGC CCCTAGAACA ACCAGTATTA 780

	GAAGGTGCCA CCATTGGTGC TGCCTTCTCT TCCACAGCC TGTAACCTAG TGTTTTGTAC	840
5	TTCACTGAAT TGTGATGGTT AGAACTTCG TGGATAGTTT GTGGAAATCA TCCAATTAAA	900
	CATACTGCTT AAAACAGTGT TGCTGTGACT TCAGAGACAA GCCTGGAAGG GGCACCTTAG	960
	GAAGCCCCTT CGCTTCAGTT GCTCGCTTCT GGGTGTGCTC CCTTCGAAGG CCCAGATAAG	1020
10	ACAGGGAACA CTTGTGAGCA CACAGAGCAG CATCTGATGC CCTGTGGTGT TTGGCATGTG	1080
	CCCCCTGTCT ACTGACCAAT CAGTGTGGCA TGAGGCCAC GCCACCCAAA CCTTTCACCT	1140
15	TCCAAAGAGC TAGCCGTCCT CCACCCAGTA CCATGTCCTA GCCTGTCTGC ATTTGTTAGT	1200
	GGTAATATTC TTTATGTATA ATAAATTTT ATACCCAAGC CATTGATGTA CTTTTCCTTG	1260
	TACTCTCCCT TGTGGGTCCC TTGTCTGGCT TGGCTGAACC CCAAAATGCT TTGGGGTTGG	1320
20	ACAGACCTGG CTGAACCTTA GTTCTTCAT CTATGAAATG GGAATATGAA TTAATGCAGC	1380
	AGCTTTTAGG GCAGATTGTC CATGGCATAT ACAAGGTAAC TACCATAGTG CTCCTTGGGT	1440
25	ATTGCCAATA TCCTATTATT TCTGTGTAAT ATGAAGATAC TGATTGTTTT GAG	1493

30 (2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 577 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

40	AATTGGCAG AGGNATTATA TAACTATAC TGGCATTAC TGTTCACCC AGCCCGGAAA	60
	GTCAGAGATG TATATTGAA AATTACAAC TCCATCTACA TTGGTTCCA GGACGCTCTC	120
	ATAGCACATT ACCCAAGAAT CTACAACGAT GATAAGAACA CCTATATTCT TTATGAACTT	180
45	GAATATATCT TATAATTTTA TTGTTTATTT TGTGTTAAT GCACAGCTAC TTCACACCTT	240
	AACTTGCTT TGATTGGTG ATGTAACTT TTAAACATTG CAGATCAGTG TAGAACTGGT	300
50	CATAGAGGAA GAGCTAGAAA TCCAGTAGCA TGATTTTAA ATAACCTGTC TTTGTTTTTG	360
	ATGTTAAACA GTAAATGCCA GTAGTGACCA AGAACACAGT GATTATATAC ACTATACTGG	420
	AGGGATTTC TTTTAAATC ATCTTTATGA AGATTTAGAA CTCATTCTT GTGTTTAAAG	480
55	GGAATGTTTA ATTGAGAAAT AAACATTTGT GWACAAAATG YTAACAAAAA AAAAAAAA	540
	AAAAAAA AAAAAAAA AAAAAAAA AACTCGA	577

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2860 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GTGTNGACCG CTCTCNCAAT ATGGCTCCCC CGGGCTGGCA GRWRKTCRGT CWCKRGTTGGC 60
TAGCCTGTCC TGACAGGGGA GAGTTAAGCT CCCGTTCTCC ACCGTGCCGG CTGGCCAGGT 120
15 GGGCTGAGGG TGACCGAGAG ACCAGAACCT GCTTGCTGGA GCTTAGTGCT CAGAGCTGGG 180
GAGGGAGGTT CCGCCGCTCC TCTGCTGTCA GCGCCGGCAG CCCCTCCCGG CTTCACTTCC 240
20 TCCCCGAGCC CCGCTACTG AGAAGCTCCG GGATCCCGAG AGCCGCCACG CCCTGGCCTC 300
AGCCTGCGGG GCTTCCAGTC AGGCCAACAC CGACGCGCAC TGGGGAGGAA GACAGGACCC 360
TTGACATCTC CATCTGCACA GAGGTCTCTG CTGGAACCGA GCAGCCTCCT CCTCCTAGGA 420
25 TGACCTCACC CTCCAGCTCT CAGTTTTC A GGTGAGAC ATTAGATGGA GGCCAAGAAG 480
ATGGCTCTGA GCGGACAGA GGAAAGCTGG ATTTTGGGAG CGGGCTGCCT CCCATGGAGT 540
30 CACAGTTCCA GGGCGAGGAC CGGAAATTCG CCCCTTCAGA TAAGAGTCAA CCTCCAACTA 600
CCGAAAGGGA ACAGGTGCCA GTCAGCCGGA TCCAAACCGA TTTGACCGAG ATCGGCTCTT 660
CAATGCGGTC TCCCGGGGTG TCCCCGAGGA TCTGGCTGGA CTTCAGAGT ACCTGAGCAA 720
35 GACCAGCAAG TACCTACCG ACTTCGAAA TACACAGAGG GCTCCACAGG TAAGACGGCC 780
TGATGAAGGC TGTGCTGAAA CCTTAAGGAC GGGGTCAATG CTTGCATTCT GCCACTGCTG 840
40 CAGATCGACC GGAATCTGG CAATCCTCAG CCCCTGGTAA ATGCCAGTG CACAGATGAC 900
TATTACGAG GCCACAGCGC TCTGCACATC GCCATTGAGA AAGAGGAGTC TGCAGTGTGT 960
GAAGCTCCTG GTGGAGAATG GGGCCAATGT GCATGCCCGG GTCTGCGGCG ACTTCTTCCA 1020
45 GAAGGGCCAA GGGACTTGCT TTTATTTTCG TGAGCTACCC CTCTCTTTGG CCGCTTGAC 1080
CAAGCAGTGG GATGTGGTAA GCTACCTCCT GGAGAACCCA CACCAGCCCG CCAGCCTGCA 1140
50 GGCCACTGAC TCCAGGGCA ACACAGTCCT GCATGCCCTA GTGGATGATC TCGGACAACT 1200
CAGCTGAGAA CATTGCACTG GTGACCAGCA TGTATGATGG CCTCCTCCAA GCTKGGGSCC 1260
SCCYTCTGCC CTACCGTCCA GCTTGAGGAC ATCCGCAACC TGCAGGATCT CACGCCTCTG 1320
55 AAGCTGGCCG CCAAGGAGGG CAAGATCGAG ATTTTCAGGC ACATCCTGCA GCGGGAGTTT 1380
TCAGGACTGA GCCACCTTTC CCGAAAGTTC ACCGAGTGCT GCTATGGGCC TGTCCGGGTG 1440
60 TCGCTGTATG ACCTGGCTTC TGTGGACAGC TGTGAGGAGA ACTCAGTGCT GGAGATCATT 1500

	GCCTTTCATT GCAAGAGCCC GCACCGACAC CGAATGGTCG TTTTGGAGCC CCTGAACAAA	1560
5	CTGCTGCAGG CGAAATGGGA TCTGCTCATC CCCAAGTTCT TCTTAAACTT CCTGTGTAAT	1620
	CTGATCTACA TGTCATCTT CACCGCTGTT GCCTACCATC AGCCTACCCT GAAGAAGCAG	1680
	GCCGCCCCCTC ACCTGAAAGC GGAGGTTGGA AACTCCATGC TGCTGACGGG CCACATCCTT	1740
10	ATCCTGCTAG GGGGGATCTA CCTCCTCGTG GGGCCAGCTG TGGTACTTCT GGCGGCGCCA	1800
	CGTGTTCATC TGGATCTCGT TCATAGACAG CTACTTTGGA AATCCTCTTC CTGTTCCAGG	1860
	CCCTGCTTCA CAGTGGTGTC CCAGGTGCTG TGTTCCTGG GCCATCGAGT GGTACCTGCC	1920
15	CCTGCTTGTC TCTGCGCTGG TGGCTGGGCT GGCTGAACCT GCTTTACTAA TACACGTGGC	1980
	GTTCACGAC ACAGGCAGTC TACAGTTTCA TGWTCCCTGA AGCCCTGGTG AGCCTGAGCC	2040
20	AGGAGGCTTG GCGCCCCGAA GCTCCTACAG GCCCCAATGC CACAGAGTCA GTGCAGCCCA	2100
	TGGAGGGACA GGAGGACGAG GGCAACGGG CCCAGTACAG GGTATCCTG GAAGCCTCCT	2160
	TGGAGCTCTT CAAATTCACC ATCGGCATGG GCGAGCTGGC CTTCCAGGAG CAGCTGCACT	2220
25	TCCGCGGCAT GGTGCTGCTG CTGCTGCTGG CCTACGTGCT GCTCACCTAC ATCCTGCTGC	2280
	TCAACATGCT CATCGCCCTC ATGAAGCGAA CGTCACAGTG TCGCCACTGA CAGCTGGAGC	2340
30	ATCTGGAAGC TGCAGAAAGC CATCTCTGTC CTGGAGATGG AGAATGGCTA TTGGTGGTGC	2400
	AGGAAAAAGC AGCGGGCAGG TGTGATGCTG ACCGTTGGCA CTAAGCCCAG ATGGCAGCCC	2460
35	CGATGAGCGC TGGTGCTTCA GGGTGGAGGA GGTGAACTGG GCTTCATGGG GAGCAGACGC	2520
	TGCTACGCT GTGTGAGGAC CCGTCAGGGG CAGGTGTCCC TCGAACTCTC GAGAACCCTG	2580
	TCCTGGCTTC CCCTCCCAAG GAGGATGAGG ATGGTGCCTC TGAGGAAAAC TATGTGCCCG	2640
40	TCCAGTCTCT CCAGTCCAAC TGATGGCCCA GATGCAGCAG GAGGCCAGAG GACAGAGCAG	2700
	AGGATCTTTC CAACCACATC TGCTGGCTCT GGGGTCCCAG TGAATTCTGG TGGCAAATAT	2760
45	ATATTTTCAC TAACTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAVGAGGG GGGGCCCKT	2820
	ASCCAAWTC GCCCTATAAG TGAGTGCCWA TTACGATAAA	2860

50

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CTGCTTGTGT CTGCGCTGGT GCTGGGCTGG CTGAACCTGC TTTACTATAC ACGTGGCTTC 60
 CAGCACACAG GCATCTACAG TGTCTGATC CAGAAGCCCT GGTGAGCCTG AGCCAGGANN 120
 5 TTGGCGCCCC GAAGCTCCTA CAGGCCCCAA TGCCACAGAG TCAGTGCAGC CCATGGAGGG 180
 ACAGGAGGAC GAGGGCAACG GGGCCAGTA CAGGGGTATC CTGGAAGCCT CCTTGGAGCT 240
 10 CTTCAAATTC ACCATCGGCA TGGCGAGCT GGCCTTCCAG GAGCAGCTGC ACTTCCGCGG 300
 CATGGTGTG CTGCTGCTGC TGGCCTACGT GCTGCTCACC TACATCCTGC TGCTCAACAT 360
 GCTCATCGCC CTCATGNAGC GAGACCGWCA ACAGTGTCCG CACTGACAGC TGGAGCATCT 420
 15 GGAAGCTGCA GAAAGCCATC TCTGTCTTGG AGATGGAGAA TGGCTATTGG TGGTGCAGGA 480
 AGAAGCAGCG GGCAGGTGTG ATGCTGACCG TTGGCACTAA GCCAGATGCC AGCCCCGATG 540
 AGCCTGGTG CTTCAAGGTG GAGGAGGTGA ACTGGGCTTC ATGGGAGCAG ACGCTGCCTA 600
 20 CGCTGTGTGA GGACCCGTC GGGCAGGTG TCCCTCGAAC TCTCGAGAAC CCTGTCTTGG 660
 CTTCCCTCC CAAGGAGGAT GAGGATGGTG CTTCTGAGGA AAATATGTG CCCGTCCAGC 720
 25 TCCTCCAGTC CAACTGATGG CCCAGATGCA GCAGGAGGCC AGAGGACAGA GCAGAGGATC 780
 TTTCCAACCA CATCTGCTGG CTCTGGGGTC CCAGTGAATT CTGGTGGCAA ATATATATTT 840
 TCACTAAMWM AAAAAAAAAA AAAAAAAAAA ACTCGA 876
 30

35 (2) INFORMATION FOR SEQ ID NO: 309:
 40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

45 CATGACCCGC CTGATGCGAT CCCGCACAGC CTCTGGTTCC AGCGTCACTT CTCTGGATGG 60
 CACCCGCAGC CGCTCCACA CCAGCGAGGG CACCCGAAGC CGCTCCACA CCAGCGAGGG 120
 CACCCGCAGC CGCTCGACA CCAGCGAGGG GGCCACCTG GACATCACC CCAACTCGGG 180
 50 TGCTGCTGGG AACASGCCGG GCCCAAGTCC ATGGAGGTCT CTTGCTAGGC GGCCTGCCCA 240
 GCTGCCGCCC CCGACTCTG ATCTCTGTAG TGGCCCCCTC CTCCCCGGCC CCTTTTCGCC 300
 CCCTGCCTGC CATACTGCGC CTAATCGGT ATTAATCCAA AGCTTATTTT GTAAGAGTGA 360
 55 GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC TCTCCAAAGG CGGGGTGGCG 420
 GTGGACCAA GGAAGGAAGC AAGCATCTCC GCATCGCATC CTCTCCATT AACCAAGTGGC 480
 60 CGGTGGCCAC TCTCTCCCC TCCCTCAGAG ACACCAAAT GCCAAAAACA AGACGCGTAC 540

AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCCTGAGC ATCCTGGTTC AAACGGGTGC 600
 CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTCTCTCTTT AACTGAGGAG AAGCTGATCC 660
 5 AGTTTCCGGA AACAAAATCC TTTTCTCATT TGGGGAGGGG GGTAAATAGTG ACATGCAGGC 720
 ACCTCTTTTA AACAGGCAAA ACAGGAAGGG GGAAAAGGTG GGATTCATGT CGAGGCTAGA 780
 10 GGCATTTGGA ACAACAAATC TACGTAGTTA ACTTGAAGAA ACCGATTTTT AAAGTTGGTG 840
 CATCTAGAAA GCTTTGAATG CAGAAGCAAA CAAGCTTGAT TTTTCTAGCA TCCTCTTAAT 900
 GTGCAGCAAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG ACAAAAATAT TTCAGCAAAAC 960
 15 GTTGGGCATC ATGGTTTTTG AAGGCTTTAG TTCTGCTTTC TGCCTCTCCT CCACAGCCCC 1020
 AACCTCCAC CCCTGATACA TGAGCCAGTG ATTATTCTTG TTCAGGGAGA AGATCATTTA 1080
 20 GATTTGTTTT GCATTCTTA GAATGGAGGG CAACATTCCA CAGCTGCCCT GGCTGTGATG 1140
 AGTGTCTTTC CAGGGGCCCG AGTAGGAGCA CTGGGGTGGG GGCGGAATTG GGGTTACTCG 1200
 ATGTAAGGGA TTCCTTGTG TTGTGTGAG ATCCAGTGCA GTTGTGATTT CTGTGGATCC 1260
 25 CAGCTTGGTT CCAGGAATTT TGTGTGATTG GCTTAAATCC AGTTTTCAAT CTTCGACAGC 1320
 TGGGCTGGAA CGTGAATCA GTAGCTGAAC CTGTCTGACC CGGTACGTT CTGGATCCT 1380
 30 CAGAACTCTT TGCTCTTGTG GGGGTGGGG TGGAACTCA CGTGGGAGC GGTGGCTGAG 1440
 AAAATGTAAG GATTCTGGAA TACATATTCC ATGGGACTTT CCTTCCCTCT CTGCTTCCT 1500
 CTPTTCTGTC TCCCTAACCT TTCGCCGAAT GGGGCAGCAC CACTGACGTT TCTGGGCGGC 1560
 35 CAGTGGCGCT GCCAGGTTCC TGTACTACTG CTTGTACTTT TTCATTTTGG CTCACCGTGG 1620
 ATTTTCTCAT AGGAAGTTG GTCAGAGTGA ATTGAATATT GTAAGTCAGC CACTGGGACC 1680
 40 CGAGGATTTT TGGGACCCCG CAGTTGGGAG GAGGAAGTAG TCCAGCCTTC CAGGTGGCGT 1740
 GAGAGGCAAT GACTCGTTAC CTGCCGCCCA TCACCTTGA GGCCTTCCCT GGCCTTGAGT 1800
 AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGAGTACGGA TGGGAACTA TTGTGCACAA 1860
 45 GTCTTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA TTTCAGACC AATAAATTTG 1920
 TAACTTTGCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAATC 1980
 50 GAGGGGGGCC CGTACCCAAT TCGCCGTATA TGATCGTAAA CAATC 2025

55 (2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3026 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

5	TAGGCAGCAC TGAATATATCC TAACCCCTTA AGCTCCAGGT GCCCTGTGGN ACGAGCAACT	60
	GGACTATAGC AGGGCTGGGC TCTGTCTTCC TGGTCATAGG CTCACTCTTT CCCCCAAATC	120
	TTCTCTGGA GCTTTCAGC CAAGGTGCTA AAAGGAATAG GTAGGAGACC TCTTCTATCT	180
10	AATCCTTAAA AGCATAATGT TGAACATTCA TTCAACAGCT GATGCCCTAT AACCCCTGCC	240
	TGGATTTCCTT CCTATTAGGC TATAAGAAGT AGCAAGATCT TTACATAATT CAGAGTGGTT	300
15	TCATGCGCTT CCTACCCCTCT CTAATGGCCC CTCCATTTAT TTGACTAAAG CATCACACAG	360
	TGGCACTAGC ATTATACCAA GAGTATGAGA AATACAGTGC TTTATGGCTC TAACATTACT	420
	GCCCTCAGTA TCAAGGCTGC CTGGAGAAAAG GATGGCAGCC TCAGGGCTTC CTTATGTCCT	480
20	CCACCACAAG AGCTCCTTGA TGAAGGTCAT CTTTTTCCTC TATCCTGTTC TTCCCTCTCC	540
	CGCTCCTAAT GGTACGTGGG TACCCAGGCT GGTCTTGGG CTAGGTAGTG GGGACCAAGT	600
25	TCATTACCTC CCTATCAGTT CTAGCATAGT AACTACGGT ACCAGTGTTA GTGGGAAGAG	660
	CTGGGTTTTC CTAGTATACC CACTGCATCC TACTCCTACC TGGTCAACCC GCTGCTTCCA	720
	GGTATGGGAC CTGCTAAGTG TGAATTACC TGATAAGGA GAGGGAAATA CAAGGAGGGC	780
30	CTCTGGTGT CTGGCCTCA GCCAGCTGCC CACAAGCCAT AAACCAATAA AACAAGAATA	840
	CTGAGTCAGT TTTTATCTG GGTCTCTTC ATTCCACTG CACTTGGTGC TGCTTTGGCT	900
35	GACTGGGAAC ACCCCATAAC TACAGAGTCT GACAGGAAGA CTGGAGACTG TCCACTTCTA	960
	GCTCGAACT TACTGTGTAA ATAACTTTC AGAACTGCTA CCATGAAGTG AAAATGCCAC	1020
	ATTTTGCTTT ATAATTTCTA CCCATGTTGG GAAAACTGG CTTTTCCTCA GCCCTTTCCA	1080
40	GGGCATAAAA CTCAACCCCT TCGATAGCAA GTCCCATCAG CCTATTATTT TTTTAAAGAA	1140
	AACCTGCACT TGTTCCTCT TTTACAGTTA CTTCCTTCCT GCCCCAAAT TATAAACTCT	1200
45	AAGTGTAATA AAAAGTCTTA ACAACAGCTT CTGCTTGTA AAAATATGTA TTATACATCT	1260
	GTATTTTAA ATTCTGCTCC TGAAAAATGA CTGTCCCAT CTCCACTCAC TGCATTTGGG	1320
	GCCCTTCCCA TTGGTCTGCA TGTCTTTTAT CATTCAGGC CAGTGGACAG AGGAGAAGG	1380
50	GAGAACAGGG GTCGCAACA CTTGTGTTGC TTTCTGACTG ATCCTGAACA AGAAAGAGTA	1440
	ACACTGAGGC GCTGCTCCC ATGCACAACT CTCCAAAACA CTTATCCTCC TGCAAGAGTG	1500
55	GGCTTTCCAG GGTCTTTACT GGAAGCAGT TAAGCCCCCT CTCACCCCT TCCTTTTTC	1560
	TTTCTTTACT CCTTTGGCTT CAAAGGATTT TGGAAAAGAA ACAATATGCT TTACTCAT	1620
60	TTTCAATTT TAAATTTGCA GGGGATACTG AAAAATACGG CAGGTGGCCT AAGGCTGCTG	1680

	TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT TACAAGATAA AAAACGAATC CCCTAAACAA	1740
	AAAGAACAAT AGAACTGGTC TTCCATTTTG CCACCTTTCC TGTTCATGAC AGCTACTAAC	1800
5	CTGGAGACAG TAACATTTCA TTAACCAAAG AAAGTGGGTC ACCTGACCTC TGAAGAGCTG	1860
	AGTACTCAGG CCACTCCAAT CACCCACAA GATGCCAAGG AGGTCCCAGG AAGTCCAGCT	1920
10	CCTTAAACTG ACGCTAGNMA ATAAACCTGG GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT	1980
	CCATCTGTGA GGTGAYAGGC AAGGATGAAA GACAAAGAAG GAAAAGAGTA TCAAAGGCAG	2040
	AAAGGAGATC ATTTAGTTGG GTCTGAAAGG AAAAGTCTTT GCTATCCGAC ATGTACTGCT	2100
15	AGTACCTGTA AGCATTTTAG GTCCCAGAAT GGAAAAAAA ATCAGCTATT GGTAATATAA	2160
	TAATGTCCTT TCCCTGGAGT CAGTTTTTTT AAAAAGTTAA CTCTTAGTTT TTACTTGTTT	2220
20	AATTCTAAAA GAGAAGGGAG CTGAGGCCAT TCCCTGTAGG AGTAAAGATA AAAGGATAGG	2280
	AAAAGATTCA AAGCTCTAAT AGAGTCACAG CTTTCCAGG TATAAACCT AAAATTAAGA	2340
	AGTACAATAA GCAGAGGTGG AAAATGATCT AGTTCCTGAT AGCTACCCAC AGAGCAAGTG	2400
25	ATTTATAAAT TTGAAATCCA AACTACTTTC TTAATATCAC TTTGGTCTCC ATTTTTCCTCA	2460
	GGACAGGAAA TATGTCCCCC CCTAACTTTC TTGCTTCAAA AATTAAAATC CAGCATCCCA	2520
30	AGATCATTCT ACAAGTAATT TTGCACAGAC ATCTCTTCAC CCCAGTGCCT GTCTGGAGCT	2580
	CACCCAAGGT CANCCAAACA ACTTGGTTGT GAACCAACT GCCTTAACCT TCTGGGGGAG	2640
	GGGGATTAGC TAGACTAGGA GACCCAGAAG TGAATGGGAA AGGGTGAGGA CTTCACAATG	2700
35	TTGGCCTGTC AGAGCTTGAT TAGAAGCCAA GACAGTGCCA GCAAAGGAAG ACTTGGCCCA	2760
	GGAAAAACCT GTGGGTGTG CTAATTTCTG TCCAGAAAAT AGGGTGAGCA GAAGCTTGTG	2820
40	GGGTGCATGG AGGAATGGG ACCTGGTTAT GTTGTATTTC TCGGACTGTG AATTTTGGTG	2880
	ATGTAAAACA GAATATTCTG TAAACCTAAT GTCTGTATAA ATAATGAGCG TTAACACAGT	2940
	AAAATATTCA ATAAGAAGTC AAAAAAAAAA AAAAAAACT CGAGGGGGGG CCCGGTACCC	3000
45	AATTTNCCAA ATAGAGATNG TATTAC	3026

50 (2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 712 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

60 GCAGGCTTTG TGCTCACCTA CAAGCTGGGT GAGCAGGGTG CCAGCAGCCT GTTTCCTCTT 60

CTCTGCTGG ACCACGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG TGTGGGTGCT 120
 GTGGTCTGCT CCATGCTGG CTCTCCCTG GGTGGGACCT TGCTGGCCAA GCACTGGAAA 180
 5 CTGCTGCCTC TGTGTARGTC GGTGCTGCGC TTCCGCTCG GGGCCCTAGC CTGTCAGACT 240
 GCCTTGGTCT TCCACCTGGA CACCCTGGGG GCCAGCATGG ACGCTGGCAC AATCTTGAGA 300
 10 GGGTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GAGGCCTGGT CACCACAGTC 360
 ACCTTCACTG GGATGATGCG CTGCAGCCAG CTGGCCCCCA GGGCCTGCAG GCCACACACT 420
 ACAGCCTTCT GGCCACGCTG GAGCTGCTGG GGAAGCTGCT COTGGGCACT CTGCGGAGGC 480
 15 CTGGCTGATG GGTGGGGGCC ACATCCCTGC TTCTTGCTCC TGCTCATCCT CTCTGCCTTT 540
 CCGTTCCTGT ACCTGGACCT AGCACCCAGC ACCTTCTCTT GAGCTGAGTG GCTGGAGTGG 600
 20 TCAATAAAGC CACATGTGCC TGTGGCCCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 660
 AACTGGAGGG GGGGCCCGGT ACCCAAATCG CCGGATATGA TCGTAAACAA TC 712

25

(2) INFORMATION FOR SEQ ID NO: 312:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CAAAATTTC AACTTTCAG GAGGGCAAGA GAATATCAA CAAAGATTT TGAAGTATT 60
 TTGCCAACCT TCTGGTTGAG CTGCAAGAAA ATATTTATGG TGAGAACTTT TCTGTTTCCC 120
 40 GTTATTGGGT TTTTGGTTGG TTTTGTGTTG TTTTITACTA TGCTTTGGTC TGTAAAAATA 180
 TGCAACTGAA CTACATTCAG AAGGAAATAT TGTCTACATA GAATATTATA TGAAGTTGGT 240
 45 ACATAATTCT GATGAGGAAA AAAAATCTTT GCAATTCTTT AAGCCATATT GTTGTTTTTC 300
 TGTGTTGTTT TCCCTGGATG AAAATATCAG TATTAAGTAG ACAGCATATT ATTCAAGTGT 360
 TTAGACTTAT TAATATGTTT TTGTCCTGTA TTTATACATA TGTGTATTTT GGAAAGTATT 420
 50 GCCTTTTITA AGGGAAGCTA TAATTCGATA CATAGTGAAA AAGGGAATGG TGACCCCTTT 480
 GTGCCTCTTC CACTGAGGAT AACAAACAGC ATTGTAATCC ATTCTCTTGC ACCTTCTTCT 540
 55 TCTTATCTTG TTATTACGGT TTTATTAATT TTGTAGAGGG ACAGGGAGTG GGCAAGGGGA 600
 AGAAGCAGCT TATTTGACTA ACCAGCCCCT CTGTGGTCCA CCAGCGTCTT GGCTTGGTGG 660
 GAGGGCTCTC AATCAGCAGG GCCCCAGGAG GGAAGAAGAA GTGGGGCAA GCCTGGCCTC 720
 60

GCGGCTCGGG AGCTTTGCCA TCTGAGCCAC GCCTCCTCCA GGCCATGCTC CTTGAACCTTG 780
 GAAATGTCAA CCGGAGCCCT TACACCAGCC CTCCAGCATC TAATAGACTT GAATCTACTC 840
 5 TAAACGAATA TTTAATCCAA CCTCACTACA TTGTAGCTCA GTCCAACGAC TAACCCTGAA 900
 ATGGGGGTGT TCCAGCCTTC AGCGAGATGG CCAAGCGGTC CCCTGGGGGC TGTGGCAGCG 960
 GGCTTATCCT TCTCTGTGTC CAACCTTGCC GTCCGACCTC CTCGCCCCC ATGCGGTGAC 1020
 10 CCCGTCCGTG TCTGTGTCTG TCCATACGTG TGAGTCCAGC TAAAAAGACA AAACAGAACC 1080
 CGTGGGCCCA GCTCGGAAGG TGC GTGGAGA AGGCTCCGAC GTCTCCGAAG TGCAGCCCTT 1140
 15 GGGATGGCAT TCCGTGTGT GCCTTATTCC TGGAGAATCT GTATACGGCT CGCCTATAGA 1200
 AATATAGCCT CTTTATGCTG TATTAAAAGG ACTTTTAAAA GCAAAAAAAA AAAAAAAAAA 1260
 CTTGAGGGGG GGNCCGGTAC CCAATTNTC 1289
 20

25 (2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Ile Leu Phe Ser Ser Ser
 1 5 10 15

35 Leu Pro Phe Leu Trp Leu
 20

40 (2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Met Phe Leu Thr Gln Gly Gly Pro Leu Pro Ser Thr Arg Ala Arg
 1 5 10 15

50 Pro Thr Cys Gln Ala Gly Ala Leu Pro Lys Pro Ser Gly Leu Leu Gly
 20 25 30

55 Val Thr Cys Trp Asn Gly Leu Lys Gly Pro Leu Cys Gly Asn Arg Cys
 35 40 45

Ser Pro Asn Thr Leu Leu Leu Ala Ala Arg Gln Ala Leu Trp Lys Gly
 50 55 60

60 Arg Gly Arg Thr His Gln Asp Leu Pro Gly Pro Leu Gln Gly Arg Gln

65 70 75 80

Leu Gly Pro Glu Pro Lys His Leu Ala Leu Leu Pro Pro Arg Gly Gln
 85 90 95

5

Glu Ala Ser Trp Ala Ser Ser Leu Pro Gly Gln Gly Pro Leu Pro Leu
 100 105 110

Pro His Ile Asn Cys Thr Val Phe Ser Leu Lys Ala Ser Phe Ile Lys
 115 120 125

10

15

(2) INFORMATION FOR SEQ ID NO: 315:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

25 Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu
1 5 10 15
Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser
20 25

30

(2) INFORMATION FOR SEQ ID NO: 316:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

40

Met Asp Gly Phe Ser Ser Arg Leu Phe Ser Ser Leu Pro Phe Val Ala
1 5 10 15

Leu Gln Trp Phe Ile Val Ile Ser His Leu Leu Ser Leu Ser Leu Ser
45 20 25 30

Ala Cys Cys Tyr Gln Thr His Cys Ser Leu Xaa Gln Leu Ser Ser Ala
35 40 45

50 Phe Ser Xaa Met Gly Glu Ser Cys Val Gly Glu Arg Glu Tyr Xaa Phe
 50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 317:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

5

Met Pro Leu Ile Asn Leu Leu Leu Leu Tyr Tyr Val Pro Asn Gly Gly
 1 5 10 15

10

Lys Gln Asp Lys Lys
 20

(2) INFORMATION FOR SEQ ID NO: 318:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Gly Arg His Leu Val Leu Val Met Phe Ile Thr Thr Ser Leu His
 1 5 10 15

25

Ser Gly Thr Pro Val Pro Glu Asn Val Ile Cys Gly Val Thr Lys Gly
 20 25 30

Pro Gln Gly Lys Lys Lys Lys
 35

30

(2) INFORMATION FOR SEQ ID NO: 319:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

40

Met Leu Trp Trp Ser Arg Asp Tyr Thr Met Val Phe Leu Leu Phe Thr
 1 5 10 15

45

Met Val Phe Thr Gly Asp Leu Val Ile Arg Gly Arg Thr Glu Leu Ser
 20 25 30

Leu

50

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

60

Met Val Cys Ser Ser Leu Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe

1 5 10 15
 Ile Val Phe Arg Leu Arg Glu Val Trp Gln Ala Leu Pro Leu Ile Leu
 20 25 30
 5 Phe Ala Val Leu Gly Leu Leu Ala Ala Gly Val Thr Leu Leu Leu Pro
 35 40 45
 10 Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Met Lys Asp Ala Glu Asn
 50 55 60
 Leu Gly Arg Lys Ala Lys Pro Lys Glu Asn Thr Ile Tyr Leu Lys Val
 65 70 75 80
 15 Gln Thr Ser Glu Pro Ser Gly Thr
 85

20 (2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Gln Pro Gly Ala Gly Val Leu Val Leu Gly Leu Leu Leu Pro Pro
 1 5 10 15
 30 Pro Gln Ser Pro Ser Leu Ser
 20

35 (2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Thr Phe Thr Leu Gly Asp Ser Gln Val Leu Leu Ile Asn Leu Phe
 1 5 10 15
 45 Pro Ser Met Pro Ser Gly Ser Cys Ala Arg Pro
 20 25

50 (2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

60 Met Cys Leu Glu Cys Trp Ala Glu Asn Leu Gly Pro His His Thr Ser

1 5 10 15
 Ser Leu Leu Asn Pro Arg His Leu Pro Ser Ile Pro Ala Met Phe Pro
 20 25 30
 5 Val Ser Ser Gly Cys Phe Gln Glu Gln Glu Met Asn Lys Ser Leu
 35 40 45
 10 Val Ser Cys Leu Phe Val Leu His Phe Val Leu His Cys Ile Phe Xaa
 50 55 60

15

(2) INFORMATION FOR SEQ ID NO: 324:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

25 Met Leu Ser Thr Ser Glu Tyr Ser Gln Ser Pro Lys Met Glu Ser Leu
 1 5 10 15
 Ser Ser His Arg Ile Asp Glu Asp Gly Glu Asn Thr Gln Ile Glu Asp
 20 25 30
 30 Thr Glu Pro Met Ser Pro Val Leu Asn Ser Lys Phe Val Pro Ala Glu
 35 40 45
 35 Asn Asp Ser Ile Leu Met Asn Pro Ala Gln Asp Gly Glu Val Gln Leu
 50 55 60
 Ser Gln Asn Asp Asp Lys Thr Lys Gly Asp Asp Thr Asp Thr Arg Asp
 65 70 75 80
 40 Asp Ile Ser Ile Leu Ala Thr Gly Cys Lys Gly Arg Glu Glu Thr Val
 85 90 95
 Ala Glu Glu Val Cys Ile Asp Leu Thr Cys Asp Ser Gly Ser Gln Ala
 100 105 110
 45 Val Pro Ser Pro Ala Thr Arg Ser Glu Ala Leu Ser Ser Val Leu Asp
 115 120 125
 Gln Glu Glu Ala Met Glu Ile Lys Glu His His Pro Glu Glu Gly Ser
 50 130 135 140
 Ser Gly Ser Glu Val Glu Glu Ile Pro Glu Thr Pro Cys Glu Ser Gln
 145 150 155 160
 55 Gly Glu Glu Leu Lys Glu Glu Asn Met Glu Ser Val Pro Leu His Leu
 165 170 175
 Ser Leu Thr Glu Thr Gln Ser Gln Gly Leu Cys Leu Arg Arg His Pro
 180 185 190
 60

Lys Lys Lys Lys
195

5

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

10 Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg Lys
15 1 5 10 15
Arg Leu Leu Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu
20 20 25 30
Ala Xaa Xaa Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp
25 35 40 45
Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr
25 50 55 60
Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val
30 65 70 75 80
Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val
35 85 90 95
Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys
100 105 110
Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp
35 115 120 125
Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln
40 130 135 140
Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala
145 150 155 160
Ala Arg Xaa His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg
45 165 170 175
Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser Met
180 185 190
Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln Asn
50 195 200 205
Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu Ala
55 210 215 220
Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly Pro
225 230 235 240
Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa
60 245 250

(2) INFORMATION FOR SEQ ID NO: 326:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val
1 5 10 15

15

Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Ala Pro Ala
20 25 30

Val Ile Lys Asn Asn Ser His Tyr Gln Thr Ser Lys Ala Leu Glu Leu
35 40 45

20

Glu Lys Thr Thr Glu Asn Lys Glu Ser Asn Pro Phe Ile Leu Gln Val
50 55 60

Asn Lys Leu Xaa
65

25

(2) INFORMATION FOR SEQ ID NO: 327:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Gly Glu Gly Lys Asn Gly Phe Gly Gly Phe Val His Thr Ala Asp
1 5 10 15

40

Ala Cys Trp Glu Gly Val His Ser Glu Pro Val Cys Arg Thr Val His
20 25 30

Thr Val His Thr Cys His His Gln Ala Phe Leu Val Leu Ile Gly Trp
35 40 45

45

Ser Lys Ser Gly Lys Glu Arg Lys Glu Ala Phe Leu Thr Ala Ile Ile
50 55 60

Leu Asn Ser Arg Ser Ile His Ile Ser Cys Ser Trp Pro Pro Ser Pro
65 70 75 80

50

Val Pro Gln Xaa

55

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

5 Met Leu Leu Ile Asn Leu Leu Trp Leu Val Thr Met Ile Lys Ser Val
 1 5 10 15
 Ile Asn Asn Asn Ile Ile Leu Phe Leu Lys Lys Lys Ser Leu Phe Phe
 20 25 30
 10 Ile Asp Ser Val
 35

15

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

25 Met Thr Phe Pro Phe Glu Lys Lys Ile Val Ala Phe Ser Ala Phe Tyr
 1 5 10 15
 Leu Ile Pro Gly Glu Ser Arg Leu Ala Pro Thr Phe Asn Pro Ser Ala
 20 25 30
 30 Asp Met Thr Val Ile Leu Arg Gly Arg Ala Gln His Lys Thr Ala Met
 35 40 45
 Leu Glu Ser Tyr Asn Trp Lys Val Ser Cys Gln Leu Arg Glu Xaa
 50 55 60
 35

(2) INFORMATION FOR SEQ ID NO: 330:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

45

Met His Ser Lys Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile
 1 5 10 15
 50 Leu Ile Leu Pro Val Cys Ala His Leu His Glu Glu Leu Asn Cys Cys
 20 25 30
 Phe His Arg
 35

55

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

5 Met Gly Ala Leu Val Leu Leu Leu Cys Leu Leu Val Gly Val Gln Gln
 1 5 10 15

Ser Gly Ser Val Trp Asp Ser
 20

10

(2) INFORMATION FOR SEQ ID NO: 332:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

20

Met Gln Ser Ala Glu Ile Leu Ser Trp Thr Asp Val Leu His Asp Phe
 1 5 10 15

25

Leu Phe Ser Leu Phe Leu Trp Pro Ala Phe Glu Asp Arg Ala Leu Leu
 20 25 30

Ile Phe Thr Leu Asn Gln Ile Val
 35 40

30

(2) INFORMATION FOR SEQ ID NO: 333:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

40 Met Gln Ser Leu Val Gln Trp Gly Leu Asp Ser Tyr Asp Tyr Leu Gln
 1 5 10 15

Asn Ala Pro Pro Gly Phe Phe Pro Arg Leu Gly Val Ile Gly Phe Ala
 20 25 30

45

Gly Leu Ile Gly Leu Leu Leu Ala Arg Gly Ser Lys Ile Lys Lys Leu
 35 40 45

50

Val Tyr Pro Pro Gly Phe Met Gly Leu Ala Ala Ser Leu Tyr Tyr Pro
 50 55 60

Gln Gln Ala Ile Val Phe Ala Gln Val Ser Gly Glu Arg Leu Tyr Asp
 65 70 75 80

55

Trp Gly Leu Arg Gly Tyr Ile Val Ile Glu Asp Leu Trp Lys Glu Asn
 85 90 95

Phe Gln Lys Pro Gly Asn Val Lys Asn Ser Pro Gly Thr Lys Xaa
 100 105 110

60

(2) INFORMATION FOR SEQ ID NO: 334:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Ala Pro Ser Leu Leu Leu Ala Pro Leu Cys Ser Leu Glu Ala
 1 5 10 15

15

Val Leu Ser Ser Pro Leu Glu Lys Gln Cys Gln Leu Pro Gly Ile Phe
 20 25 30

Cys Gln Leu Gln Leu Pro Cys Pro Leu Leu Leu Ser Ala Gln Leu Leu
 35 40 45

20

Lys Gly Ile Val Xaa Pro Arg Cys Pro Ala Ser Leu Pro Gln Pro Pro
 50 55 60

His Pro Ala Pro Ser Trp His Leu Pro Leu His Cys Thr Glu Arg Xaa
 65 70 75 80

25

Pro His His Leu Pro Leu Gln Gly Gly Ser Ser Asn Met Glu Glu Xaa
 85 90 95

30

Asn Tyr Arg Gly Tyr Xaa Asp Ala Gln Leu
 100 105

(2) INFORMATION FOR SEQ ID NO: 335:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Thr Thr Cys Leu Phe Gly Leu Leu Ser Cys Glu Met Ser Ala Gln
 1 5 10 15

45

Val Ser Gln Lys Ser Cys Val Tyr Asp Glu Ser Glu Cys Phe Ser Ser
 20 25 30

Val Gly Gln Leu Leu Ala Leu Leu Ile Leu Val Tyr Val Leu Pro Ser
 35 40 45

50

Ile Xaa
 50

55

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

5 Met Leu Trp Lys Cys Ser Gln Asn Ile Ala Arg Cys Leu Leu Leu Leu
 1 5 10 15
 Leu Ala Leu Val Glu Ile Lys Leu Glu Asp Leu Gln Ser Gln Leu His
 20 25 30
 10 Pro Thr Trp Lys Ser Ile Pro Gly Pro Ser Pro Arg Asn Gln His Arg
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 337:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

25 Met Leu Ile Pro Leu Gln Cys Leu Phe Ser Ser Asp Arg Met Leu Thr
 1 5 10 15
 30 Phe Leu Thr Pro Trp Gln Lys Gly Glu Lys Cys Val Leu Gly Trp Val
 20 25 30
 Thr Lys Phe Leu Ser Glu Ile Ser Xaa
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 338:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

45 Met Thr Phe Ser Ser Leu Lys Leu Phe Val Leu Thr Cys Ile Ile Lys
 1 5 10 15
 Gly Leu Glu Arg Phe Ile Ile Leu Arg Glu Val Cys Asn Gln Glu Ile
 20 25 30
 50 Gln Arg Ser Leu Ser Ser Asn Leu Val His Val Leu Leu Gln Pro Ala
 35 40 45
 55 Thr Phe Lys Asp Val Leu Val Thr Glu Ile Ile Cys Leu Cys Met Cys
 50 55 60
 Leu Tyr Ser Ile Lys Tyr Met Pro Pro Gln Lys Lys
 65 70 75

60

(2) INFORMATION FOR SEQ ID NO: 339:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

10 Lys Val Tyr Ile Phe Leu Ile Phe Met Val Leu Ile Leu Pro Ser Leu
 1 5 10 15
 Gly Leu Thr Arg Tyr Met Pro Pro Xaa Ser Xaa Leu Asn Ser Glu
 20 25 30
 15

(2) INFORMATION FOR SEQ ID NO: 340:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

25 Met Ala Lys Ile Ser Pro Phe Glu Val Val Lys Arg Thr Ser Val Pro
 1 5 10 15
 30 Val Leu Val Gly Leu Val Ile Val Ile Val Ala Thr Glu Leu Met Val
 20 25 30
 Pro Gly Thr Ala Ala Ala Val Thr Gly Lys
 35 40
 35

(2) INFORMATION FOR SEQ ID NO: 341:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

45 Met Arg Leu Phe Phe Ile Gly Phe Leu Leu Leu Phe Ser Phe Gly Leu
 1 5 10 15
 Leu Arg Gln Pro Ser Leu Ser Ala Glu His
 20 25
 50

(2) INFORMATION FOR SEQ ID NO: 342:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

60

Met Val Phe Ser Val Ser Ser Ala Leu Ala Leu Leu Leu Met Leu Leu
 1 5 10 15

5 Arg Ser Ser Asp Leu Ala Lys Lys Thr Glu
 20 25

10 (2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Ser Leu Glu Phe Tyr Gln Lys Lys Lys Ser Arg Trp Pro Phe Ser
 1 5 10 15

20 Asp Glu Cys Ile Pro Trp Glu Val Trp Thr Val Lys Val His Val Val
 20 25 30

Ala Leu Ala Thr Glu Gln Glu Arg Gln Ile Cys Arg Glu Lys Val Gly
 35 40 45

25 Glu Lys Leu Cys Glu Lys Ile Ile Asn Ile Val Glu Val Met Asn Arg
 50 55 60

30 His Glu Tyr Leu Pro Lys Met Pro Thr Gln Ser Glu Val Asp Asn Val
 65 70 75 80

Phe Asp Thr Gly Leu Arg Asp Val Gln Pro Tyr Leu Tyr Lys Ile Ser
 85 90 95

35 Phe Gln Ile Thr Asp Ala Leu Gly Thr Ser Val Thr Thr Thr Met Arg
 100 105 110

Arg Leu Ile Lys Asp Thr Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly
 115 120 125

40 Ser Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu
 130 135 140

45 Gly Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp Xaa
 145 150 155

50 (2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Phe Leu Leu Pro Leu Pro Ala Ala Gly Arg Val Val Val Arg Arg
 1 5 10 15

60 Leu Ala Val Arg Arg Phe Gly Ser Arg Ser Leu Ser Thr Ala Asp Met

	20	25	30
	Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp Asp		
	35	40	45
5	Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu Ala		
	50	55	60
10	Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys Ala		
	65	70	75 80
	Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser Val		
	85	90	95
15	Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln Glu		
	100	105	110
	Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala Gly		
	115	120	125
20	Cys Arg Gln Ile Gln Asp Leu Glu Leu Ser Ser Val Glu Val Asp Pro		
	130	135	140
25	Cys Gly Asp Ala Gln Ala Ala Ala Glu Gly Ala Val Leu Gly Leu Tyr		
	145	150	155 160
	Glu Tyr Asp Asp Leu Lys Gln Lys Lys Lys Met Ala Val Ser Ala Lys		
	165	170	175
30	Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu Phe		
	180	185	190
	Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala Asn		
	195	200	205
35	Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu Lys		
	210	215	220
40	Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp Ile		
	225	230	235 240
	Glu Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser Asp		
	245	250	255
45	Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn Ala		
	260	265	270
	Asn Glu Pro Pro Leu Val Phe Val Gly Lys Gly Ile Thr Phe Asp Ser		
	275	280	285
50	Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg Ala		
	290	295	300
55	Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala Ala		
	305	310	315 320
	Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys Glu		
	325	330	335
60	Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg Ala		

340 345 350
 Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly Arg
 355 360 365
 5 Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro Lys
 370 375 380
 Xaa Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala Leu
 10 385 390 395 400
 Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp Asn
 405 410 415
 15 Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg Met
 420 425 430
 Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu Ala
 20 435 440 445
 Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr Ala
 450 455 460
 25 Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His Leu
 465 470 475 480
 Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu Arg
 485 490 495
 30 Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu Leu
 500 505 510
 Arg Phe Ser Gln Asp Asn Ala Xaa
 35 515 520

(2) INFORMATION FOR SEQ ID NO: 345:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Thr Ile Leu Phe Leu Phe Leu Gln Leu Ser Ala Leu Arg Leu Ile Val
 1 5 10 15

50 Gly Lys Asp Ser Ile Asp Ile Asp Ile Ser Ser Arg Arg Arg Glu Asp
 20 25 30

Gln Ser Leu Arg Leu Asn Ala
 35

55

(2) INFORMATION FOR SEQ ID NO: 346:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 amino acids

560

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

5 Met Thr Ser Glu Leu Asp Ile Phe Val Gly Asn Thr Thr Leu Ile Asp
 1 5 10 15
 Glu Asp Val Tyr Arg Leu Trp Leu Asp Gly Tyr Ser Val Thr Asp Ala
 20 25 30
 10 Val Ala Leu Arg Val Arg Ser Gly Ile Leu Glu Gln Thr Gly Ala Thr
 35 40 45
 Ala Ala Val Leu Gln Ser Asp Thr Met Asp His Tyr Arg Thr Phe His
 15 50 55 60
 Met Leu Glu Arg Leu Leu His Ala Pro Pro Lys Leu Leu His Gln Leu
 65 70 75 80
 20 Ile Phe Gln Ile Pro Pro Ser Arg Gln Ala Leu Leu Ile Glu Arg Tyr
 85 90 95
 Tyr Ala Phe Asp Glu Ala Phe Val Arg Glu Val Leu Gly Lys Lys Leu
 100 105 110
 25 Ser Lys Gly Thr Lys Lys Asp Leu Asp Asp Ile Ser Thr Lys Thr Gly
 115 120 125
 Ile Thr Leu Lys Ser Cys Arg Arg Gln Phe Asp Asn Phe Lys Arg Val
 30 130 135 140
 Phe Lys Val Val Glu Glu Met Arg Gly Ser Leu Val Asp Asn Ile Gln
 145 150 155 160
 35 Gln His Phe Leu Leu Ser Asp Arg Leu Ala Arg Asp Tyr Ala Ala Ile
 165 170 175
 Val Phe Phe Ala Asn Asn Arg Phe Glu Thr Gly Lys Lys Lys Leu Gln
 180 185 190
 40 Tyr Leu Ser Phe Gly Asp Phe Ala Phe Cys Ala Glu Leu Met Ile Gln
 195 200 205
 Asn Trp Thr Leu Gly Pro Val Asp Ser Gln Met Asp Asp Met Asp Met
 45 210 215 220
 Asp Leu Asp Arg Asn Phe Ser Arg Thr Xaa
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

60 Met Ala Ala Ala Val Ala Gly Met Leu Arg Gly Gly Leu Leu Pro Gln

1 5 10 15
 Ala Gly Arg Leu Pro Thr Leu Gln Thr Val Arg Tyr Gly Ser Lys Ala
 20 25 30
 5 Val Thr Arg His Arg Arg Val Met His Phe Gln Arg Gln Lys Leu Met
 35 40 45
 10 Ala Val Thr Glu Tyr Ile Pro Pro Lys Pro Ala Ile His Pro Ser Cys
 50 55 60
 Leu Pro Ser Pro Pro Ser Pro Pro Gln Glu Glu Ile Gly Leu Ile Arg
 65 70 75 80
 15 Leu Leu Arg Arg Glu Ile Ala Ala Val Phe Gln Asp Asn Arg Met Ile
 85 90 95
 Ala Val Cys Gln Asn Val Ala Leu Ser Ala Glu Asp Lys Leu Leu Ile
 100 105 110
 20 Ala Thr Pro Ala Ala Glu Thr Gln Asp Pro Asp Glu Gly Leu Pro Gln
 115 120 125
 25 Pro Gly Pro Glu Ser Pro Ser Trp Arg Ile Pro Ser Thr Lys Ile Cys
 130 135 140
 Cys Pro Phe Leu Trp Gly Thr Thr Cys Cys Trp Ser Val Lys Ser Pro
 145 150 155 160
 30 Arg Ser Arg Arg Trp Tyr Gly Ser Xaa
 165

35 (2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Lys Arg Ser Phe Leu Leu Pro Leu Leu Leu Val Gly Phe Leu Asp
 1 5 10 15
 45 Thr Ala His Leu Ile Leu Leu Glu Thr Leu Ser Val Cys Leu Trp Leu
 20 25 30
 50 Pro Ser Leu Ile Asp Ser Arg Cys Val Met Ser
 35 40

55 (2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Lys Glu Gly Pro Cys Lys Arg His His Tyr Tyr Gln Asn Cys
 1 5 10 15
 5 Gly Ala Lys Leu Leu Val Ser Leu Phe Gly Glu Thr Asn Gln Ile His
 20 25 30
 Leu Leu Glu Thr Gln Val Gly Thr Glu Lys Gly Gly Glu Arg Ile Trp
 35 40 45
 10 Glu Glu Lys Trp Arg Ile Ser Ser Thr Val Leu Phe Ile Ser Val Asn
 50 55 60
 Ser Tyr Val Glu Gly Ser Val Leu Glu Ile Lys Leu Phe Tyr
 15 65 70 75

20 (2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Ser Glu Ile Leu Ser Leu Leu Phe Cys Leu Leu Gly Pro Ala Leu
 1 5 10 15
 30 Asp Glu Arg Arg Glu Glu Lys Asp
 20

35 (2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu
 1 5 10 15
 45 Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser
 20 25 30
 Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu
 50 35 40 45
 Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val
 50 55 60
 55 Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu
 65 70 75 80
 Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly
 85 90 95
 60

Arg Pro Ala Gly Gly Ala His Leu Cys Ala Met Xaa Val Ile Glu Gly
 100 105 110
 5 Leu Val Val Asp Val Gly Glu Arg Ile Leu His Gly Gln Arg Glu Val
 115 120 125
 Gly Gln Val Ser Gln Val Leu Pro Ala Leu Ser Leu Gly Leu Val Phe
 130 135 140
 10 Leu Cys Gln Gly Thr Val Glu Lys Val Ser Gly Ala Ala His Cys Ser
 145 150 155 160
 Ser Leu Leu Cys Cys Leu Pro Trp Gln Cys Ser Gly Gly Gly Phe Pro
 165 170 175
 15 Thr Xaa Arg Cys Ser Arg Pro Tyr Phe Ser Ser His Lys Gly Val Ala
 180 185 190
 20 Ala Thr Leu Ala Leu Thr Cys His Cys Asp Lys Val His Val Ala Gly
 195 200 205
 Leu Gly Lys Asp Trp Ala Ile Glu Gln Arg Arg Arg Thr Cys Glu Ser
 210 215 220
 25 Asp Xaa Glu Xaa Xaa Pro Phe Thr Leu Ala Gly Leu Val Leu Val Leu
 225 230 235 240
 Arg Phe Cys Gln Val Val Leu Val Trp Ile Pro Gln Leu Gly Asp Lys
 245 250 255
 30 His Trp Arg Gly Met Thr Arg Leu Gly Arg Val Ser Leu Thr Ser Ser
 260 265 270
 35 Ile Xaa

40 (2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Ile Phe Thr Ser Val Thr Lys Gly Ile Leu Leu Ile Ala Leu Trp
 1 5 10 15

50 Val Pro Leu Phe His Phe Met Leu Ile Asp Ser Ile Leu Gly Pro Ser
 20 25 30

Arg Leu Leu Thr Asp Gly Val Pro Phe Asn Pro Trp His Val Xaa
 35 40 45

55

(2) INFORMATION FOR SEQ ID NO: 353:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

5

Met Lys Thr

1

10

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

20

Met Ser Ile Ser Gly Thr Asp Gly Leu Ile Leu Leu Val Gly Leu
1 5 10 15Glu Ala Xaa Val Arg Ser Ser Lys Lys Trp Ile Pro Lys Ala Leu Xaa
20 25 30

25

Val Thr Gln Ala Lys Trp Asn Ser Trp Pro Ser Arg Arg Asn Ala Gly
35 40 45Phe Ala Leu His
50

30

(2) INFORMATION FOR SEQ ID NO: 355:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

40

Met Glu His Cys Leu Tyr His Ser Val His Gly Ile Asn Pro Tyr Ile
1 5 10 15

45

His Lys Asn Thr His Pro Ser Ile Asn Ile Tyr Met Val Trp Asp Glu
20 25 30Gln Val Asn Ser Phe Glu Arg Glu Phe Val Pro Phe Phe Phe Leu Ile
35 40 45

50

Ile Leu Leu Asn Cys Cys Gln Leu Ser Asn Lys Gln Thr Glu Lys Leu
50 55 60Phe Gly Lys Thr Leu His Thr Pro Phe Leu Ser Ser Ala Leu Lys Tyr
65 70 75 80

55

Arg Leu Asn Thr His Ile Leu Pro Val Phe Ser Tyr Ser Asp Ser Ile
85 90 95

60

Leu Thr Cys His Leu Ile Leu Ala Ser Tyr Phe Ser His Val Tyr Leu
100 105 110

Pro Val Thr Cys Ile Cys Tyr Leu Asn Arg Lys Lys Asn Ile Gln Lys
 115 120 125

5 Lys Lys Asn Xaa
 130

10 (2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly Ser Arg Asp His Leu Phe Lys Val Leu Val Val Gly Asp Ala
 1 5 10 15
 20 Ala Val Gly Lys Thr Ser Leu Val Gln Asp Tyr Ser Gln Asp Ser Phe
 20 25 30
 25 Ser Lys His Tyr Lys Ser Thr Val Gly Val Asp Phe Ala Leu Lys Val
 35 40 45
 Leu Gln Trp Ser Asp Tyr Glu Ile Val Arg Leu Gln Leu Trp Asp Ile
 50 55 60
 30 Ala Gly Gln Glu Arg Phe Thr Ser Met Thr Arg Leu Tyr Tyr Arg Asp
 65 70 75 80
 Ala Ser Ala Cys Val Ile Met Phe Asp Val Thr Asn Ala Thr Thr Phe
 85 90 95
 35 Ser Asn Ser Gln Arg Trp Lys Gln Asp Leu Asp Ser Lys Leu Thr Leu
 100 105 110
 40 Pro Asn Gly Glu Pro Val Pro Cys Leu Leu Leu Ala Asn Lys Cys Asp
 115 120 125
 Leu Ser Pro Trp Ala Val Ser Arg Asp Gln Ile Asp Arg Phe Ser Lys
 130 135 140
 45 Glu Asn Gly Phe Thr Gly Trp Thr Glu Thr Ser Val Lys Glu Asn Lys
 145 150 155 160
 Asn Ile Asn Glu Ala Met Arg Val Leu Ile Glu Lys Met Met Arg Asn
 165 170 175
 50 Ser Thr Glu Asp Ile Met Ser Leu Ser Thr Gln Gly Asp Tyr Ile Asn
 180 185 190
 55 Leu Gln Thr Lys Ser Ser Ser Trp Ser Cys Cys Xaa
 195 200

60 (2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ile Ser Leu Ile Phe Gln Leu Glu Glu Glu Lys Leu Val Glu Lys
 1 5 10 15

10 Phe Phe Phe Phe Leu Phe Phe Phe Leu Lys Lys Gly Ser Gln Gly Ser
 20 25 30

Asn Leu Lys Ile Val Pro Arg His Met Arg Val Val Leu Arg Gly
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 358:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Thr Tyr Val Thr Cys Leu His Val Cys Leu Leu Val Glu Phe Leu
 1 5 10 15

30 Asn Ser Gln Leu Thr Asn His Arg Lys Tyr Tyr Phe Leu Ser Tyr Gly
 20 25 30

Phe Trp Phe Thr Gly Leu Arg Gly Phe Ser Glu Tyr Leu Trp Pro Gln
 35 40 45

35 Gln His Thr Ser Phe His Pro Asn Arg Asn Glu Ile Asn Phe Val Ser
 50 55 60

Thr Asp Asn Arg Ile Trp Val Thr Xaa
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 359:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Ser Asp Gln Glu Ala Lys Pro Ser Thr Glu Asp Leu Gly Asp Lys
 1 5 10 15

55 Lys Glu Gly Glu Tyr Ile Lys Leu Lys Val Ile Gly Gln Asp Ser Ser
 20 25 30

Glu Ile His Phe Lys Val Lys Met Thr Thr His Leu Lys Lys Leu Lys
 35 40 45

60 Glu Ser Tyr Cys Gln Arg Gln Gly Val Pro Met Asn Ser Leu Arg Phe

15

(D) TOPOLOGY: linear

20

30

(2) INFORMATION FOR SEQ ID NO: 361:

(D) TOPOLOGY: linear

55

[illegible]

Arg His Leu Ser Val Val Thr Leu Ala Ala Lys Val Lys Cys Ile Pro
 100 105 110

5 Tyr Ala Val Leu Leu Glu Ala Leu Ala Leu Arg Asn Val Arg Gln Leu
 115 120 125

Glu Asp Leu Val Ile Glu Ala Val Tyr Ala Asp Val Leu Arg Gly Ser
 130 135 140

10 Leu Asp Gln Arg Asn Gln Arg Leu Glu Val Asp Tyr Ser Ile Gly Arg
 145 150 155 160

15 Asp Ile Gln Arg Gln Asp Leu Ser Ala Ile Ala Arg Thr Leu Xaa Lys
 165 170 175

Asn His Xaa

20

(2) INFORMATION FOR SEQ ID NO: 362:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

30 Met Lys Ser Ser Ser Leu Phe Phe Phe Phe Leu Ala His Phe Ile His
 1 5 10 15

Ser His Asp Leu Pro Gly Leu Cys Arg
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 363:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

45 Met Lys Phe Ala Ala Ser Gly Xaa Phe Leu His His Met Ala Gly Leu
 1 5 10 15

50 Ser Ser Ser Lys Leu Ser Met Ser Lys Ala Leu Pro Leu Thr Lys Val
 20 25 30

Val Gln Asn Asp Ala Tyr Thr Ala Pro Ala Leu Pro Ser Ser Ile Arg
 35 40 45

55 Thr Lys Ala Leu Thr Asn Met Ser Arg Thr Leu Val Asn Lys Glu Glu
 50 55 60

Pro Pro Lys Glu Leu Pro Ala Ala Glu Pro Val Leu Ser Pro Leu Glu
 65 70 75 80

60

Gly Thr Lys Met Thr Val Asn Asn Leu His Pro Arg Val Thr Glu Glu
 85 90 95
 5 Asp Ile Val Glu Leu Phe Cys Val Cys Gly Ala Leu Lys Arg Ala Arg
 100 105 110
 Leu Val His Pro Gly Val Ala Glu Val Val Phe Val Lys Lys Asp Asp
 115 120 125
 10 Ala Ile Thr Ala Tyr Lys Lys Tyr Asn Asn Arg Cys Leu Asp Gly Gln
 130 135 140
 Pro Met Lys Cys Asn Leu His Met Asn Gly Asn Val Ile Thr Ser Asp
 145 150 155 160
 15 Gln Pro Ile Leu Leu Arg Leu Ser Asp Ser Pro Ser Met Lys Lys Glu
 165 170 175
 Ser Glu Leu Pro Arg Arg Val Asn Ser Ala Ser Ser Ser Asn Pro Pro
 180 185 190
 Ala Glu Val Asp Pro Asp Thr Ile Leu Lys Ala Leu Phe Lys Ser Ser
 195 200 205
 25 Gly Ala Ser Xaa Thr Thr Gln Pro Thr Glu Phe Lys Ile Lys Leu Xaa
 210 215 220

30

(2) INFORMATION FOR SEQ ID NO: 364:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

40

Met Ser Lys Asn Cys Ile Lys Leu Leu Cys Glu Asp Pro Val Phe Ala
 1 5 10 15

45

Glu Tyr Ile Lys Cys Ile Leu Met Asp Glu Arg Thr Phe Leu Asn Asn
 20 25 30

Asn Ile Val Tyr Thr Phe Met Thr His Phe Leu Leu Lys Val Gln Ser
 35 40 45

50

Gln Val Phe Ser Glu Ala Asn Cys Ala Asn Leu Ile Ser Thr Leu Ile
 50 55 60

Thr Asn Leu Ile Ser Gln Tyr Gln Asn Leu Gln Ser Asp Phe Ser Asn
 65 70 75 80

55

Arg Val Glu Ile Ser Lys Ala Ser Ala Ser Leu Asn Gly Asp Leu Arg
 85 90 95

60

Ala Leu Ala Leu Leu Leu Ser Val His Thr Pro Lys Gln Leu Asn Pro
 100 105 110

Ala Leu Ile Pro Thr Leu Gln Glu Leu Leu Ser Lys Cys Arg Thr Cys
 115 120 125

5 Leu Gln Gln Arg Asn Ser Leu Gln Glu Gln Glu Ala Lys Glu Arg Lys
 130 135 140

Thr Lys Asp Asp Glu Gly Ala Thr Pro Ile Lys Arg Arg Arg Val Ser
 145 150 155 160

10 Ser Asp Glu Glu His Thr Val Asp Ser Cys Ile Ser Asp Met Lys Thr
 165 170 175

Glu Thr Arg Glu Val Leu Thr Pro Thr Ser Thr Ser Asp Asn Glu Thr
 180 185 190

15 Arg Asp Ser Ser Ile Ile Asp Pro Gly Thr Glu Gln Asp Leu Pro Ser
 195 200 205

Pro Glu Asn Ser Ser Val Lys Glu Tyr Arg Met Glu Val Pro Ser Ser
 210 215 220

Phe Ser Glu Asp Met Ser Asn Ile Arg Ser Gln His Ala Glu Glu Gln
 225 230 235 240

25 Ser Asn Asn Gly Arg Tyr Asp Asp Cys Lys Glu Phe Lys Asp Leu His
 245 250 255

Cys Ser Lys Asp Ser Thr Leu Ala Glu Glu Glu Ser Glu Phe Pro Ser
 260 265 270

30 Thr Ser Ile Ser Ala Val Leu Ser Asp Leu Ala Asp Leu Arg Ser Cys
 275 280 285

35 Asp Gly Gln Ala Leu Pro Ser Gln Asp Pro Glu Val Ala Leu Ser Leu
 290 295 300

Ser Cys Gly His Ser Arg Gly Leu Phe Ser His Met Gln Gln His Asp
 305 310 315 320

40 Ile Leu Asp Thr Leu Cys Arg Thr Ile Glu Ser Thr Ile His Val Val
 325 330 335

Thr Arg Ile Ser Gly Lys Gly Asn Gln Ala Ala Ser Xaa
 340 345

45

50 (2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Leu His Gln Asp His Ile Thr Phe Ala Met Leu Leu Ala Arg Ile
 1 5 10 15

60 Lys Leu Lys Gly Thr Val Gly Glu Pro Thr Tyr Asp Ala Glu Phe Gln

	20	25	30
	His Phe Leu Arg Gly Asn Glu Ile Val Leu Ser Ala Gly Ser Thr Pro		
	35	40	45
5	Arg Ile Gln Gly Leu Thr Val Glu Gln Ala Glu Ala Val Val Arg Leu		
	50	55	60
	Ser Cys Leu Pro Ala Phe Lys Asp Leu Ile Ala Lys Val Gln Ala Asp		
10	65	70	75 80
	Glu Gln Phe Gly Ile Trp Leu Asp Ser Ser Ser Pro Glu Gln Thr Val		
	85	90	95
15	Pro Tyr Leu Trp Ser Glu Glu Thr Pro Ala Thr Pro Ile Gly Gln Ala		
	100	105	110
	Ile His Arg Leu Leu Leu Ile Gln Ala Phe Arg Pro Asp Arg Leu Leu		
20	115	120	125
	Ala Met Ala His Met Phe Val Ser Thr Asn Leu Gly Glu Ser Phe Met		
	130	135	140
	Ser Ile Met Glu Gln Pro Leu Asp Leu Thr His Ile Val Xaa Thr Glu		
25	145	150	155 160
	Val Lys Pro Asn Thr Pro Val Leu Met Cys Ser Val Pro Gly Tyr Asp		
	165	170	175
30	Ala Ser Gly His Val Glu Asp Leu Ala Ala Glu Gln Asn Thr Gln Ile		
	180	185	190
	Thr Ser Ile Ala Ile Gly Ser Ala Glu Gly Phe Asn Gln Ala Asp Lys		
35	195	200	205
	Ala Ile Asn Thr Ala Val Lys Ser Gly Arg Trp Val Met Leu Lys Asn		
	210	215	220
	Val His Leu Ala Pro Gly Trp Leu Met Gln Leu Glu Lys Lys Leu His		
40	225	230	235 240
	Ser Leu Gln Pro His Ala Cys Phe Arg Leu Phe Leu Thr Met Glu Ile		
	245	250	255
45	Asn Pro Lys Val Pro Val Asn Leu Leu Arg Ala Gly Arg Ile Phe Val		
	260	265	270
	Phe Glu Pro Pro Pro Gly Xaa Lys Ala Asn Met Leu Arg Thr Phe Ser		
50	275	280	285
	Ser Ile Pro Val Ser Arg Ile Cys Lys Ser Pro Asn Glu Arg Ala Arg		
	290	295	300
	Leu Tyr Phe Leu Leu Ala Trp Phe His Ala Ile Ile Gln Glu Arg Leu		
55	305	310	315 320
	Arg Tyr Ala Pro Leu Gly Trp Ser Lys Lys Tyr Glu Phe Gly Glu Ser		
	325	330	335
60	Asp Leu Arg Ser Xaa Cys Asp Thr Val Asp Thr Trp Leu Asp Asp Thr		

[illegible]

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

	Met	Ala	Asp	Glu	Ala	Thr	Arg	Arg	Val	Val	Ser	Glu	Ile	Pro	Val	Leu
	1				5					10					15	
40	Lys	Thr	Asn	Ala	Gly	Pro	Arg	Asp	Arg	Glu	Leu	Trp	Val	Gln	Arg	Leu
				20					25					30		
	Lys	Glu	Glu	Tyr	Gln	Ser	Leu	Ile	Arg	Tyr	Val	Glu	Asn	Asn	Lys	Asn
			35					40					45			
45	Ala	Asp	Asn	Asp	Trp	Phe	Arg	Leu	Glu	Ser	Asn	Lys	Glu	Gly	Thr	Arg
		50					55					60				
	Trp	Phe	Gly	Lys	Cys	Trp	Tyr	Ile	His	Asp	Leu	Leu	Lys	Tyr	Glu	Phe
50		65				70					75					80
	Asp	Ile	Glu	Phe	Asp	Ile	Pro	Ile	Thr	Tyr	Pro	Thr	Thr	Ala	Pro	Glu
					85					90					95	
55	Ile	Ala	Val	Pro	Glu	Leu	Asp	Gly	Lys	Thr	Ala	Lys	Met	Tyr	Arg	Gly
				100					105					110		
	Gly	Lys	Ile	Cys	Leu	Thr	Asp	His	Phe	Lys	Pro	Leu	Trp	Gly	Gln	Glu
			115					120					125			

Cys Ala Gln Ile Trp Thr Ser Ser Ser His Gly Ser Gly Ala Gly Ser
 130 135 140

5 Met Xaa Gly Ser Gly Asn Pro Xaa
 145 150

10 (2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Tyr Asp Gly Thr Lys Glu Val Pro Met Asn Pro Val Lys Ile Tyr
 1 5 10 15

20 Gln Val Cys Asp Ile Pro Gln Pro Gln Gly Ser Ile Ile Asn Pro Gly
 20 25 30

Ser Thr Gly Ser Ala Pro Trp Asp Glu Lys Asp Asn Asp Val Asp Glu
 35 40 45

25 Glu Asp Glu Glu Asp Glu Leu Asp Gln Ser Gln His His Val Pro Ile
 50 55 60

30 Gln Asp Thr Phe Pro Phe Leu Asn Ile Asn Gly Ser Pro Met Ala Pro
 65 70 75 80

Ala Ser Val Gly Asn Cys Ser Val Gly Asn Cys Ser Pro Glu Ala Val
 85 90 95

35 Trp Pro Lys Thr Glu Pro Leu Glu Met Glu Val Pro Gln Ala Pro Ile
 100 105 110

Gln Pro Phe Tyr Ser Ser Pro Glu Leu Trp Ile Ser Ser Leu Pro Met
 115 120 125

40 Thr Asp Leu Asp Ile Lys Phe Gln Tyr Arg Gly Lys Glu Tyr Gly Gln
 130 135 140

Thr Met Thr Val Ser Asn Pro Gln Gly Cys Arg Leu Phe Tyr Gly Asp
 145 150 155 160

Leu Gly Pro Met Pro Asp Gln Glu Glu Leu Phe Gly Pro Val Xaa Leu
 165 170 175

50 Glu Gln Val Lys Phe Pro Gly Pro Glu His Ile Thr Asn Glu Lys Gln
 180 185 190

Lys Leu Phe Thr Ser Lys Leu Leu Asp Val Met Asp Arg Gly Leu Ile
 195 200 205

55 Leu Glu Val Ser Gly His Ala Ile Tyr Ala Ile Arg Leu Cys Gln Cys
 210 215 220

60 Lys Val Tyr Trp Ser Gly Pro Cys Ala Pro Ser Leu Val Ala Pro Asn
 225 230 235 240

[illegible]

30

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

40 Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser
1 5 10 15

Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe
20 25 30

45 Trp Gly Phe Gly Arg Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr
35 40 45

Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser
50 55 60

50

His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln
65 70 75 80

Pro Asn Xaa

55

(2) INFORMATION FOR SEQ ID NO: 369:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala
 1 5 10 15

10 Tyr Trp Thr Met Xaa
 20

15 (2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Gly Ala Ser Ala Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro
 1 5 10 15

25 Gly Ser Gly Lys Gly Thr Val Ser Ser Arg Ile Thr Thr His Phe Glu
 20 25 30

30 Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Asp Asn Met Leu Arg
 35 40 45

Gly Thr Glu Ile Gly Val Leu Ala Lys Ala Phe Ile Asp Gln Gly Lys
 50 55 60

35 Leu Ile Pro Asp Asp Val Met Thr Arg Leu Ala Leu His Glu Leu Lys
 65 70 75 80

Asn Leu Thr Gln Tyr Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
 85 90 95

40 Pro Gln Ala Glu Ala Leu Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile
 100 105 110

45 Asn Leu Asn Val Pro Phe Glu Val Ile Lys Gln Arg Leu Thr Ala Arg
 115 120 125

Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
 130 135 140

50 Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln
 145 150 155 160

Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr
 165 170 175

55 Glu Asp Gln Thr Lys Pro Val Leu Glu Tyr Tyr Gln Lys Lys Gly Val
 180 185 190

60 Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val
 195 200 205

Tyr Ala Phe Leu Gln Thr Lys Val Pro Gln Arg Ser Gln Lys Ala Ser
 210 215 220

5 Val Thr Pro
 225

10 (2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Phe Leu Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln
 1 5 10 15
 20 Leu Lys Ile Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu
 20 25 30
 25 Lys Ile Ile Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser
 35 40 45
 Trp Ala Ile Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn
 50 55 60
 30 Lys Thr Ala Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr Xaa
 65 70 75

35 (2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ala Val Phe Pro Cys Cys Pro Phe Leu Thr Leu Met Leu Pro
 1 5 10 15
 45 Leu Leu Glu Cys Leu Val Gly Met Ile Met Cys Tyr Leu Gly Ile Ser
 20 25 30
 50 Phe Thr Asp Thr Arg Lys Thr Ala Gly Leu Lys Lys Lys Lys Lys Lys
 35 40 45
 Lys Xaa Xaa
 50

55

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 61 amino acids

577

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

5 Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser
 1 5 10 15
 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Ala Ser Tyr Leu Trp
 20 25 30
 10 Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Ser Trp Ala Cys
 35 40 45
 15 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu Xaa
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 374:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe
 1 5 10 15
 30 Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg
 20 25 30
 Ile Leu Phe Phe Ile Val Phe Xaa
 35 40
 35

(2) INFORMATION FOR SEQ ID NO: 375:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Cys Ser Gly Gln Ser Gln Val Trp Lys Met Ala Leu Gln Ala Leu
 1 5 10 15
 50 Asp Ser Glu Thr Val Val Ile Leu Pro Asp Met His Leu Ile Leu Ser
 20 25 30
 Leu Arg Leu Ile His Asn Ala Arg Pro Cys Leu Xaa
 35 40

55

(2) INFORMATION FOR SEQ ID NO: 376:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

5 Met Leu Ile Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp Pro Arg Asp
 1 5 10 15

Glu Thr Tyr Lys Pro His Leu Glu Arg Glu Thr Pro Lys Pro Arg Arg
 20 25 30

10 Lys Ser Gly Lys Val Lys Glu Glu Lys Glu Lys Lys Glu Ile Lys Val
 35 40 45

Glu Val Glu Val Glu Val Lys Glu Glu Glu Asn Glu Ile Arg Glu Asp
 15 50 55 60

Glu Glu Pro Pro Arg Lys Arg Gly Arg Arg Arg Lys Asp Asp Lys Ser
 65 70 75 80

20 Pro Arg Leu Pro Lys Arg Arg Lys Lys Pro Pro Ile Gln Tyr Val Arg
 85 90 95

Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His Pro Arg Tyr Leu
 100 105 110

25 Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys Lys Tyr Val Cys
 115 120 125

Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys Gln Leu Leu
 130 135 140

Arg His Ala Lys His His Thr Asp Gln Arg Asp Tyr Ile Cys Glu Tyr
 145 150 155 160

35 Cys Ala Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met
 165 170 175

Ile His Thr Gly Glu Lys His Tyr Asn Val Arg Ser Val Asp Leu Leu
 180 185 190

40 Val Asp Lys Arg His Leu Leu Ile Gly Thr Xaa
 195 200

45

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

55 Met Leu Pro Arg Arg Thr Phe Tyr Phe Tyr Phe Ile Phe Ile Phe Phe
 1 5 10 15

Leu Ala Ser Phe Trp Gly Phe Thr Leu Arg Ala Ser Phe
 20 25

60

(2) INFORMATION FOR SEQ ID NO: 378:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

10 Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu Met
 1 5 10 15
 Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val Leu
 20 25 30
 15 Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu Trp
 35 40 45
 20 Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg Met
 50 55 60
 Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val Gln
 65 70 75 80
 25 Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu Asn
 85 90 95
 Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met Pro Ser Phe
 100 105 110
 30 Phe Ser Cys His Leu Phe Cys Thr Leu Arg Trp Lys Tyr Phe Glu Val
 115 120 125
 Phe Tyr Asn His Lys Phe Leu Xaa
 130 135
 35

(2) INFORMATION FOR SEQ ID NO: 379:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Ala Trp Arg Arg Arg Glu Pro Ala Ser Gly Leu Ala Ala Cys Trp
 1 5 10 15
 50 Leu Trp Arg Cys Ser Pro Trp Pro Cys Ala Cys Pro Gly Pro Gly Ala
 20 25 30
 Gly Leu Ser Ser Gly Ser Arg Pro Trp
 35 40
 55

(2) INFORMATION FOR SEQ ID NO: 380:

- 60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

5 Met Glu Phe Leu Lys Val Ala Arg Arg Asn Lys Arg Glu Gln Leu Glu
 1 5 10 15
 10 Gln Ile Gln Lys Glu Leu Ser Val Leu Glu Glu Asp Ile Lys Arg Val
 20 25 30
 Glu Glu Met Ser Gly Leu Tyr Ser Pro Val Ser Glu Asp Ser Thr Val
 35 40 45
 15 Pro Gln Phe Glu Ala Pro Ser Pro Ser His Ser Ser Ile Ile Asp Ser
 50 55 60
 Thr Glu Tyr Ser Gln Pro Pro Gly Phe Ser Gly Ser Ser Gln Thr Lys
 65 70 75 80
 20 Lys Gln Pro Trp Tyr Asn Ser Thr Leu Ala Ser Arg Arg Lys Arg Leu
 85 90 95
 25 Thr Ala His Phe Glu Asp Leu Glu Gln Cys Tyr Phe Ser Thr Arg Met
 100 105 110
 Ser Arg Ile Ser Asp Asp Ser Arg Thr Ala Ser Gln Leu Asp Glu Phe
 115 120 125
 30 Gln Glu Cys Leu Ser Lys Phe Thr Arg Tyr Asn Ser Val Arg Pro Leu
 130 135 140
 Ala Thr Leu Ser Tyr Ala Ser Asp Leu Tyr Asn Gly Ser Ser Ile Val
 145 150 155 160
 35 Ser Ser Ile Glu Phe Asp Arg Asp Cys Asp Tyr Phe Ala Ile Ala Gly
 165 170 175
 40 Val Thr Lys Lys Ile Lys Val Tyr Glu Tyr Asp Thr Val Ile Gln Asp
 180 185 190
 Ala Val Asp Ile His Tyr Pro Glu Asn Glu Met Thr Cys Asn Ser Lys
 195 200 205
 45 Ile Ser Cys Ile Ser Trp Ser Ser Tyr His Lys Asn Leu Leu Ala Ser
 210 215 220
 Ser Asp Tyr Glu Gly Thr Val Ile Leu Trp Asp Gly Phe Thr Gly Gln
 225 230 235 240
 50 Arg Ser Lys Val Tyr Gln Glu His Glu Lys Arg Cys Trp Ser Val Asp
 245 250 255
 Phe Asn Leu Met Asp Pro Lys Leu Leu Ala Ser Gly Ser Asp Asp Ala
 260 265 270
 55 Lys Val Lys Leu Trp Ser Thr Asn Leu Asp Asn Ser Val Ala Ser Ile
 275 280 285
 60 Glu Ala Lys Ala Asn Val Cys Cys Val Lys Phe Ser Pro Ser Ser Arg

581

290 295 300

Tyr His Leu Ala Phe Gly Cys Ala Asp His Cys Val His Tyr Tyr Asp
305 310 315 320

5 Leu Arg Asn Thr Lys Gln Pro Ile Met Val Phe Lys Gly His Arg Lys
325 330 335

Ala Val Ser Tyr Ala Lys Phe Val Ser Gly Glu Glu Ile Val Ser Ala
10 340 345 350

Ser Thr Asp Ser Gln Leu Lys Leu Trp Asn Val Gly Lys Pro Tyr Cys
355 360 365

15 Leu Arg Ser Phe Lys Gly His Ile Asn Glu Lys Asn Phe Val Gly Leu
370 375 380

Ala Ser Asn Gly Asp Tyr Ile Ala Cys Gly Ser Glu Asn Asn Ser Leu
20 385 390 395 400

Tyr Leu Tyr Tyr Lys Gly Leu Ser Lys Thr Leu Leu Thr Phe Lys Phe
405 410 415

25 Asp Thr Val Lys Ser Val Leu Asp Lys Asp Arg Lys Glu Asp Asp Thr
420 425 430

Asn Glu Phe Val Ser Ala Val Cys Trp Arg Ala Leu Pro Asp Gly Glu
435 440 445

30 Ser Asn Val Leu Ile Ala Ala Asn Ser Gln Gly Thr Ile Lys Val Leu
450 455 460

Glu Leu Val Xaa
35 465

(2) INFORMATION FOR SEQ ID NO: 381:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Arg Lys Glu Asp Gly Phe Trp Phe Phe Phe Leu Phe Phe
1 5 10 15

Val Val Gly Ser Lys Phe Val Asn Gly Asn Lys Leu Val
20 25

55 (2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Pro Leu Ala Pro Tyr Cys Asp Leu Leu Val Ala Leu Ser Phe Ala
 1 5 10 15

5 Leu Val Leu Glu Ser Pro Val Asp Ser Ser Asp Phe Thr
 20 25

10 (2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Asn Ser Leu Val Ser Trp Gln Leu Leu Leu Phe Leu Cys Ala Thr
 1 5 10 15
 20 His Phe Gly Glu Pro Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg
 20 25 30
 25 Pro Thr Gly Gln Gln Leu Glu Ser Leu Gly Leu Leu Ala Pro Gly Glu
 35 40 45
 Gln Ser Leu Pro Cys Thr Glu Arg Lys Pro Ala Ala Thr Ala Arg Leu
 50 55 60
 30 Ser Arg Arg Gly Thr Ser Leu Ser Pro Pro Pro Glu Ser Ser Gly Ser
 65 70 75 80
 Pro Gln Gln Pro Gly Leu Ser Ala Pro His Ser Arg Gln Ile Pro Ala
 85 90 95
 35 Pro Gln Gly Ala Val Leu Val Gln Arg Glu Lys Asp Leu Pro Asn Tyr
 100 105 110
 40 Asn Trp Asn Ser Phe Gly Leu Arg Phe Gly Lys Arg Glu Ala Ala Pro
 115 120 125
 Gly Asn His Gly Arg Ser Ala Gly Arg Gly
 130 135

45

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

55 Met Ser Cys Phe Ile Asp Ser Xaa Asp Ser Lys Ile Leu His Leu Leu
 1 5 10 15
 Val Val Ser Phe Ile Cys Xaa Leu Phe Leu Leu Ile Leu Thr His Gly
 20 25 30
 60

Ile Leu Ile Leu Arg Xaa Phe Phe Ser Val Xaa Xaa His Ser Leu Lys
 35 40 45
 Asn Asn Leu Glu Glu Tyr Leu Ile Leu Met Asn Lys Ala Leu Leu Thr
 5 50 55 60
 Arg Glu Asp Phe Phe Val Leu Pro Xaa Ala
 65 70
 10
 (2) INFORMATION FOR SEQ ID NO: 385:
 (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 521 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:
 20 Met Ser Ala Gly Glu Val Glu Arg Leu Val Ser Glu Leu Ser Gly Gly
 1 5 10 15
 Thr Gly Gly Asp Glu Glu Glu Glu Trp Leu Tyr Gly Asp Glu Asn Glu
 20 25 30
 25 Val Glu Arg Pro Glu Glu Glu Asn Ala Ser Ala Asn Pro Pro Ser Gly
 35 40 45
 30 Ile Glu Asp Glu Thr Ala Glu Asn Gly Val Pro Lys Pro Lys Val Thr
 50 55 60
 Glu Thr Glu Asp Asp Ser Asp Ser Asp Ser Asp Asp Glu Asp Asp
 65 70 75 80
 35 Val His Val Thr Ile Gly Asp Ile Lys Thr Gly Ala Pro Gln Tyr Gly
 85 90 95
 Ser Tyr Gly Thr Ala Pro Val Asn Leu Asn Ile Lys Thr Gly Gly Arg
 100 105 110
 40 Val Tyr Gly Thr Thr Gly Thr Lys Val Lys Gly Val Asp Leu Asp Ala
 115 120 125
 45 Pro Gly Ser Ile Asn Gly Val Pro Leu Leu Glu Val Asp Leu Asp Ser
 130 135 140
 Phe Glu Asp Lys Pro Trp Arg Lys Pro Gly Ala Asp Leu Ser Asp Tyr
 145 150 155 160
 50 Phe Asn Tyr Gly Phe Asn Glu Asp Thr Trp Lys Ala Tyr Cys Glu Lys
 165 170 175
 Gln Lys Arg Ile Arg Met Gly Leu Glu Val Ile Pro Val Thr Ser Thr
 180 185 190
 55 Thr Asn Lys Ile Thr Val Gln Gln Gly Arg Thr Gly Asn Ser Glu Lys
 195 200 205
 60 Glu Thr Ala Leu Pro Ser Thr Lys Ala Glu Phe Thr Ser Pro Pro Ser
 210 215 220

Leu Phe Lys Thr Gly Leu Pro Pro Ser Arg Arg Leu Pro Gly Ala Ile
 225 230 235 240

5 Asp Val Ile Gly Gln Thr Ile Thr Ile Ser Arg Val Glu Gly Arg Arg
 245 250 255

Arg Ala Asn Glu Asn Ser Asn Ile Gln Val Leu Ser Glu Arg Ser Ala
 260 265 270

10 Thr Glu Val Asp Asn Asn Phe Ser Lys Pro Pro Pro Phe Phe Pro Pro
 275 280 285

Gly Ala Pro Pro Thr His Leu Pro Pro Pro Pro Phe Leu Pro Pro Pro
 15 290 295 300

Pro Thr Val Ser Thr Ala Pro Pro Leu Ile Pro Pro Pro Gly Phe Pro
 305 310 315 320

20 Pro Pro Pro Gly Ala Pro Pro Pro Ser Leu Ile Pro Thr Ile Glu Ser
 325 330 335

Gly His Ser Ser Gly Tyr Asp Ser Arg Ser Ala Arg Ala Phe Pro Tyr
 340 345 350

25 Gly Asn Val Ala Phe Pro His Leu Pro Gly Ser Ala Pro Ser Trp Pro
 355 360 365

Ser Leu Val Asp Thr Ser Lys Gln Trp Asp Tyr Tyr Ala Arg Arg Glu
 30 370 375 380

Lys Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp
 385 390 395 400

35 Arg Asp Arg Glu Arg Glu Arg Thr Arg Glu Arg Glu Arg Glu Arg Asp
 405 410 415

His Ser Pro Thr Pro Ser Val Phe Asn Ser Asp Glu Glu Arg Tyr Arg
 420 425 430

40 Tyr Arg Glu Tyr Ala Glu Arg Gly Tyr Glu Arg His Arg Ala Ser Arg
 435 440 445

Glu Lys Glu Glu Arg His Arg Glu Arg Arg His Arg Glu Lys Glu Glu
 45 450 455 460

Thr Arg His Lys Ser Ser Arg Ser Asn Ser Arg Arg Arg His Glu Ser
 465 470 475 480

50 Glu Glu Gly Asp Ser His Arg Arg His Lys His Lys Lys Ser Lys Arg
 485 490 495

Ser Lys Glu Gly Lys Glu Ala Gly Ser Glu Pro Ala Pro Glu Gln Glu
 500 505 510

55 Ser Thr Glu Ala Thr Pro Ala Glu Xaa
 515 520

60

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

5
10 Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu
1 5 10 15
Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val
20 25 30
15 Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu
35 40 45
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
50 55 60
20 Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr
65 70 75 80
25 Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu
85 90 95
Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr
100 105 110
30 Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly
115 120 125
Val Arg Val Phe Gly Ile Asn Lys Tyr
130 135
35

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

40
45 Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu
1 5 10 15
Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg
50 20 25 30
Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe
35 40 45
55 Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys
50 55 60
Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe
65 70 75 80
60

586

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu
85 90 95

5 Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr Leu
100 105 110

Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser Pro
115 120 125

10 Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe Trp
130 135 140

Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr Leu
145 150 155 160

15 Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val Asp
165 170 175

20 Gly Glu Glu Leu Gln Met Glu Pro Val Xaa
180 185

25 (2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met
1

35

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

45 Met Leu Ser Ile Phe Tyr Phe Ala Ile Pro Val Gly Ser Gly Leu Gly
1 5 10 15

Tyr Ile Ala Gly Ser Lys Val Lys Asp Met Ala Gly Asp Trp His Trp
20 25 30

50

Ala Leu Arg Val Thr Pro Gly Leu Gly Val Val Ala Val Leu Leu Leu
35 40 45

55 Phe Leu Val Val Arg Glu Pro Pro Arg Gly Ala Val Glu Arg His Ser
50 55 60

Asp Leu Pro Pro Leu Asn Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala
65 70 75 80

60 Leu Ala Arg Asn Pro Ser Phe Val Leu Ser Ser Leu Gly Phe Thr Ala

85 90 95

Val Ala Phe Val Thr Gly Ser Leu Ala Leu Trp Ala Pro Ala Phe Leu
100 105 110

5 Leu Arg Ser Arg Val Val Leu Gly Glu Thr Pro Pro Cys Leu Pro Gly
115 120 125

10 Asp Ser Cys Ser Ser Ser Asp Ser Leu Ile Phe Gly Leu Ile Thr Cys
130 135 140

Leu Thr Gly Val Leu Gly Val Gly Leu Gly Val Glu Ile Ser Arg Arg
145 150 155 160

15 Leu Arg His Ser Asn Pro Arg Ala Asp Pro Leu Val Cys Ala Thr Gly
165 170 175

Leu Leu Gly Ser Ala Pro Phe Leu Phe Leu Ser Leu Ala Cys Ala Arg
180 185 190

20 Gly Ser Ile Val Ala Thr Tyr Ile Phe Ile Phe Ile Gly Glu Thr Leu
195 200 205

25 Leu Ser Met Asn Trp Ala Ile Val Ala Asp Ile Leu Leu Tyr Val Val
210 215 220

Ile Pro Thr Arg Arg Ser Thr Ala Glu Ala Phe Gln Ile Val Leu Ser
225 230 235 240

30 His Leu Leu Gly Asp Ala Gly Ser Pro Tyr Leu Ile Gly Leu Ile Ser
245 250 255

Asp Arg Leu Arg Arg Asn Trp Pro Pro Ser Phe Leu Ser Glu Phe Arg
260 265 270

35 Ala Leu Gln Phe Ser Leu Met Leu Cys Ala Phe Val Gly Ala Leu Gly
275 280 285

Gly Ala Leu Pro Gly His Arg His Leu His Xaa
290 295

40

45 (2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Gly Pro Gln Gly Trp Val Arg Pro Leu Lys Thr Ala Pro Lys Leu
1 5 10 15

55 Gly Glu Ala Ile Arg Leu Ile Leu Phe Leu Asn Phe Val Lys Gln Cys
20 25 30

Ile Ala Ser Val Asn Leu Cys Ile Leu Arg Leu Asn Ile Thr Pro Leu
35 40 45

60

Leu

5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

15

Met Tyr Val Asn Tyr Gly Thr Arg Asn Tyr Ser Thr Glu Gly Pro Ala
 1 5 10 15

Ala Leu Leu Asp Gln Ala Lys Leu Ser Leu Leu Val Trp Val Leu Cys
 20 25 30

20

Phe Val Leu Leu Phe Val Cys Phe Cys Gly Leu Ser Tyr Val Val Ile
 35 40 45

25

Ala Gln Val Pro Val Gly Leu Leu Cys Ile Thr Glu Xaa
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 392:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

35

Met Leu Trp Phe Ala Asn Phe Phe Thr Tyr Leu Phe Leu Ser Gln Ser
 1 5 10 15

40

Val Ala Phe Val His Ile Ser His Ile Gly Val Arg Gln Val Asn Thr
 20 25 30

Asn Cys Tyr Phe Ser Arg Lys Ser Tyr Cys Tyr Gly Ile Leu Asn Pro
 35 40 45

45

Ile Asn Cys Ile Lys Gly Lys Lys Lys Lys Lys Lys Lys Lys
 50 55 60

50

Lys Lys Lys Lys Ile Pro Ala Gly Arg Xaa Leu Phe Pro Phe Gly
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 393:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

60

Met Pro Gly Ala Phe Ser Glu Thr Val Ile Asn Asp Leu Leu Ser Leu
1 5 10 15

5 Phe Leu Val Leu Pro Ala Glu Leu Ser Tyr Ser Thr Leu Ser Gly Val
20 25 30

Tyr Arg Asn Ala
35

10

(2) INFORMATION FOR SEQ ID NO: 394:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

20 Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
1 5 10 15

Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser
20 25 30

25

Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu
35 40 45

30 Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro
50 55 60

Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro
65 70 75 80

35 Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr
85 90 95

Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu
100 105 110

40

Leu Asp Arg Arg Ser Glu Ser Cys Ser Met Leu Pro Trp Xaa Ala Gln
115 120 125

45 Leu Leu Asp Arg Thr Ile Gly Pro Leu Tyr Leu Leu Phe Val Gln Phe
130 135 140

Ser Pro Ala Phe Ser Arg Thr Ser Pro Trp Arg Ser Pro Lys Asn Phe
145 150 155 160

50 Arg Arg Leu Tyr Pro Pro Cys Thr Thr Ser Gly Cys Ala Ala Arg Trp
165 170 175

Xaa Phe Ser Xaa
180

55

(2) INFORMATION FOR SEQ ID NO: 395:

60 (i) SEQUENCE CHARACTERISTICS:

590

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

5

Met Pro Thr Pro Cys Thr Ser Leu Pro Ser Cys Cys Gln His Arg Ser
 1 5 10 15

10

Ile Thr Met Thr Leu
 20

15

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Pro Leu Phe Ile Pro Leu Ile Phe Phe Leu Ser Leu Leu His Cys
 1 5 10 15

25

Gln Ser Lys His Pro Ile Gln Met Ser Leu Cys Met Cys Val Asn Ile
 20 25 30

30

Ser Leu Val Trp Ser Pro Val Arg Trp Ile Phe Gly Ser Lys Gly Leu
 35 40 45

Phe Ser Val His Leu Gln Ser Ser Gln Arg Pro Ser
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

45

Met Ala Gly Pro Arg Pro Xaa Trp Arg Asp Gln Leu Leu Phe Met Ser
 1 5 10 15

Ile Ile Val Leu Val Ile Val Val Ile Cys Leu Met Leu Tyr Ala Leu
 20 25 30

50

Leu Trp Glu Ala Gly Asn Leu Thr Asp Leu Pro Asn Leu Arg Ile Gly
 35 40 45

Phe Tyr Asn Phe Cys Leu Trp Asn Glu Asp Thr Ser Thr Leu Gln Cys
 50 55 60

55

His Gln Phe Pro Glu Leu Glu Ala Leu Gly Val Pro Arg Val Gly Leu
 65 70 75 80

60

Gly Leu Ala Arg Leu Gly Val Tyr Gly Ser Leu Val Leu Thr Leu Phe
 85 90 95

Ala Pro Gln Pro Leu Leu Leu Ala Gln Cys Asn Xaa Asp Glu Arg Ala
 100 105 110

5 Trp Arg Leu Ala Val Gly Phe Leu Ala Val Ser Ser Val Leu Leu Ala
 115 120 125

Gly Gly Leu Gly Leu Phe Leu Ser Tyr Val Trp Asn Gly Ser Xaa Ser
 130 135 140

10 Pro Ser Arg Gly Leu Gly Phe Xaa
 145 150

15 (2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ser Asp Gly Phe Asp Arg Ala Pro Gly Ala Gly Arg Gly Arg Xaa
 25 1 5 10 15

Arg Gly Leu Gly Arg Gly Gly Gly Gly Pro Xaa Gly Gly Gly Phe Pro
 20 25 30

30 Xaa Gly Xaa Xaa Pro Ala Glu Arg Xaa Arg His Gln Pro Pro Gln Pro
 35 40 45

Lys Ala Pro Gly Phe Leu Gln Pro Xaa Pro Leu Arg Gln Pro Arg Thr
 50 55 60

35 Thr Pro Pro Pro Gly Ala Gln Cys Glu Val Pro Ala Ser Pro Gln Arg
 65 70 75 80

Pro Ser Arg Pro Gly Ala Leu Pro Glu Gln Thr Arg Pro Leu Arg Ala
 40 85 90 95

Pro Pro Ser Ser Gln Asp Lys Ile Pro Gln Gln Asn Ser Glu Ser Ala
 100 105 110

45 Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu
 115 120 125

Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr
 130 135 140

50 Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu
 145 150 155 160

Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe
 55 165 170 175

Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr
 180 185 190

60 Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala

	195	200	205
5	Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr 210 215 220		
	Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln 225 230 235 240		
10	Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala 245 250 255		
	Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu 260 265 270		
15	Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly 275 280 285		
	Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu 290 295 300		
20	Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val 305 310 315 320		
25	Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu 325 330 335		
	Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val 340 345 350		
30	Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys 355 360 365		
	Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser 370 375 380		
35	Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn 385 390 395 400		
40	Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp 405 410 415		
	Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe 420 425 430		
45	Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp 435 440 445		
	Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu 450 455 460		
50	Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln Xaa 465 470 475 480		

55

60 (2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Glu Pro Lys Thr Ile Thr Asp Ala Leu Ala Ser Ser Ile Ile Lys
 1 5 10 15
 10 Ser Val Leu Pro Asn Phe Leu Pro Tyr Asn Val Met Leu Tyr Ser Asp
 20 25 30
 Ala Pro Val Ser Glu Leu Ser Leu Glu Leu Leu Leu Gln Val Val
 35 40 45
 15 Leu Pro Ala Leu Leu Glu Gln Gly His Thr Arg Gln Trp Leu Lys Gly
 50 55 60
 20 Leu Val Arg Ala Trp Thr Val Thr Ala Gly Tyr Leu Leu Asp Leu His
 65 70 75 80
 Ser Tyr Leu Leu Gly Asp Gln Glu Glu Asn Glu Asn Ser Ala Asn Gln
 85 90 95
 25 Gln Val Asn Asn Asn Gln His Ala Arg Asn Asn Asn Ala Ile Pro Val
 100 105 110
 Val Gly Glu Gly Leu His Ala Ala His Gln Ala Ile Leu Gln Gln Gly
 115 120 125
 30 Gly Pro Val Gly Phe Gln Xaa Tyr Arg Arg Pro Leu Asn Phe Pro Leu
 130 135 140
 35 Arg Ile Phe Leu Leu Ile Val Phe Met Cys Ile Thr Leu Leu Ile Ala
 145 150 155 160
 Ser Leu Ile Cys Leu Thr Leu Pro Val Phe Ala Gly Arg Trp Leu Met
 165 170 175
 40 Ser Phe Trp Thr Gly Thr Ala Lys Ile His Glu Leu Tyr Thr Ala Ala
 180 185 190
 Cys Gly Leu Tyr Val Cys Trp Leu Thr Ile Arg Ala Val Thr Val Met
 195 200 205
 45 Val Ala Trp Met Pro Gln Gly Arg Arg Val Ile Phe Gln Lys Val Lys
 210 215 220
 50 Glu Trp Ser Leu Met Ile Met Lys Thr Leu Ile Val Ala Val Leu Leu
 225 230 235 240
 Ala Gly Val Val Pro Leu Leu Leu Gly Leu Leu Phe Glu Leu Val Ile
 245 250 255
 55 Val Ala Pro Leu Arg Val Pro Leu Asp Gln Thr Pro Leu Phe Tyr Pro
 260 265 270
 Trp Gln Asp Trp Ala Leu Gly Val Leu His Ala Lys Ile Ile Ala Ala
 275 280 285
 60

Ile Thr Leu Met Gly Pro Gln Trp Trp Leu Lys Thr Val Ile Glu Gln
 290 295 300

5 Val Tyr Ala Asn Gly Ile Arg Asn Ile Asp Leu His Tyr Ile Val Arg
 305 310 315 320

Lys Leu Ala Ala Pro Val Ile Ser Val Leu Leu Leu Ser Leu Cys Val
 325 330 335

10 Pro Tyr Val Ile Ala Ser Gly Val Val Pro Leu Leu Gly Val Thr Ala
 340 345 350

Glu Met Gln Asn Leu Val His Arg Arg Ile Tyr Pro Phe Leu Leu Met
 355 360 365

15 Val Val Val Leu Met Ala Ile Leu Ser Phe Gln Val Arg Gln Phe Lys
 370 375 380

20 Arg Leu Tyr Glu His Ile Lys Asn Asp Lys Tyr Leu Val Gly Gln Arg
 385 390 395 400

Leu Val Asn Tyr Glu Arg Lys Ser Gly Lys Gln Gly Ser Ser Pro Pro
 405 410 415

25 Pro Pro Gln Ser Ser Gln Glu
 420

30 (2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
 1 5 10 15

40 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
 20 25 30

45 Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
 35 40 45

Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro
 50 55 60

50 Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu Xaa
 65 70 75

55 (2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser
 1 5 10 15
 5 His Cys Trp Gly Leu Pro Leu His Val Ala Pro Leu Cys Arg Gly His
 20 25 30
 10 Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala Trp
 35 40 45
 Asn Arg Asn Leu Ala Asn Gln Arg His Phe Phe Cys Pro Ser Ile Phe
 50 55 60
 15 His Thr Cys Pro Thr Val Leu Phe Phe Xaa
 65 70

20 (2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Ala Arg Thr Ile Leu Val Leu Tyr Leu Ser Leu Gln Arg Leu Glu Asn
 1 5 10 15
 30 Leu Ala Tyr His
 20

35

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

40 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Pro Leu Pro Ser Val Pro Ile Leu Gly Ile Phe Ser Phe Leu Ile
 1 5 10 15
 45 Pro Ser Ser Gln Gly Val Ser Tyr Thr Lys Leu Pro Ile Ser Ser Pro
 20 25 30
 50 Gln Tyr Ser Pro Phe Val Asn Asp His Phe Ser Phe Leu Asn Pro Phe
 35 40 45
 Pro Val Gln Ile His Thr Gly Phe Ala Arg Val Gly Ser Tyr Met Gln
 50 55 60
 55 Met Pro Leu Val His Leu Cys Leu Leu Gln Thr Ser Leu Met Lys Asn
 65 70 75 80
 60 Ser Gly Val Gln Gln Gly Ser
 85

5 (2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile Ile
1 5 10 15

15 Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala Val
20 25 30

Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile Thr
35 40 45

20 Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val Tyr
50 55 60

25 Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg Asp
65 70 75 80

Gln Thr Lys Ser Ile Val Glu Lys Ile Pro Ser Lys
85 90

30

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

40 Met Ala Cys Ser Cys Leu Met Ile Gln Ser Phe Ser Thr Ser Ala Leu
1 5 10 15

Val Leu Phe Tyr Gly
20

45

(2) INFORMATION FOR SEQ ID NO: 406:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

55

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
1 5 10 15

60 Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
20 25 30

Ser Gly Phe Pro Ala Phe Pro Lys Pro Ser Pro Thr Tyr Leu Arg Thr
 35 40 45
 5 Ser Ala Glu Gln Thr Leu Pro Leu Leu Leu Pro His Leu His Gly Leu
 50 55 60
 Cys Leu His Gln Pro Leu His Leu Gly Phe Thr Ala Cys Leu Gly Ser
 65 70 75 80
 10 Ala His Ile Leu Gly Gly Gln Pro Ala Leu Pro Ala Val Pro Glu Pro
 85 90 95
 Tyr Ala Gly His Cys Gln Arg Pro Leu Ala Gly Thr Pro His His Ser
 15 100 105 110
 Cys His Val Gly Pro Ala Asn Arg Gly Arg Arg Ser Glu Ala Trp Val
 115 120 125
 20 Gly Arg Tyr Gln Ala Ala Asn Arg Phe Pro Ile Leu Asn Ala Xaa Cys
 130 135 140
 Glu Arg Arg Thr Pro Ser Thr Val Leu Ser Ala Arg Ile Ser Ser Ala
 145 150 155 160
 25 Thr Met Gly Cys Pro Leu Phe Ala Ile Trp Ala Ala Ser Xaa
 165 170

30

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

40 Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu
 1 5 10 15
 Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His
 20 25 30
 45 Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys
 35 40 45
 Thr Glu Gly Ile Pro Cys Gln Arg Tyr Gln Asn Gly Leu His Ile Xaa
 50 55 60

50

55

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

5 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1 5 10 15
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
 20 25 30
 10 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60
 15 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95
 20 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110
 25 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
 115 120 125
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
 130 135 140
 30 His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
 145 150 155 160
 35 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
 165 170 175
 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
 180 185 190
 40 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
 195 200 205
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
 210 215 220
 45 Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
 225 230 235 240
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
 245 250 255
 50 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
 260 265 270
 55 Ile Ala Lys Val Lys Ala Asn Xaa
 275 280

60 (2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

5 Met Xaa Leu Trp Pro Gln Thr Cys Ser Gly Lys Phe Asp Gly Thr Leu
 1 5 10 15
 10 Ala Phe Ser Ile His Xaa Leu Ala Val Ile Leu Gly Asp Gln Leu Thr
 20 25 30
 15 Ala Ala Asp Leu Val Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp
 35 40 45
 Glu Val Arg Ile Gly Val Leu Lys His Leu His Asp Phe Leu Lys Leu
 50 55 60
 20 Leu His Ile Asp Lys Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe
 65 70 75 80
 Leu Val Thr Asp Asn Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala
 85 90 95
 25 Glu Gln Leu Ile Leu Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr
 100 105 110
 30 Asp Tyr Leu Arg Pro Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser
 115 120 125
 Ser Val Arg Trp Ile Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys
 130 135 140
 35 Leu His Ala Ala Thr Pro Pro Thr Phe Gly Val Asp Leu Ile Asn Glu
 145 150 155 160
 Leu Val Glu Asn Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala
 165 170 175
 40 Phe Val Phe Val Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met
 180 185 190
 45 Asp Gln Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn
 195 200 205
 Asp Arg Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln
 210 215 220
 50 Thr Leu Leu Glu Lys Asp Tyr Phe Leu Ala Ser Ala Ser Cys His Gln
 225 230 235 240
 Glu Ala Val Glu Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser
 245 250 255
 55 Asp Val Lys Tyr Phe Ala Ser Ile His Pro Ala Ser Thr Lys Ile Ser
 260 265 270
 60 Glu Asp Ala Met Ser Thr Ala Ser Ser Thr Tyr Xaa
 275 280

5 (2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Leu Phe Leu Phe Phe Val Ile Ile Phe Leu Phe Val Phe Leu Ile
1 5 10 15

15 Leu Ile Ile Gln Phe Ser Lys Pro Leu Thr Asn Pro His Pro Pro Ala
20 25 30

Gly Xaa Ser Asp Arg Arg Arg Arg Tyr Ser Ser Tyr Arg Ser His Asp
35 40 45

20 His Tyr Gln Arg Gln Arg Val Leu Gln Lys Glu Arg Ala Ile Glu Glu
50 55 60

25 Arg Arg Val Val Phe Ile Gly Lys Ile Pro Gly Arg Met Thr Arg Ser
65 70 75 80

Glu Leu Lys Gln Arg Phe Ser Val Phe Gly Glu Ile Glu Glu Cys Thr
85 90 95

30 Ile His Phe Arg Val Gln Gly Asp Asn Tyr Gly Phe Val Thr Tyr Arg
100 105 110

Tyr Ala Glu Glu Ala Phe Ala Ala Ile Glu Ser Gly His Lys Leu Arg
115 120 125

35 Gln Ala Asp Glu Gln Pro Phe Asp Leu Cys Phe Gly Gly Arg Arg Xaa
130 135 140

40 Xaa Cys Lys Arg Ser Tyr Ser Asp Leu Asp Ser Asn Arg Glu Asp Phe
145 150 155 160

Asp Pro Ala Pro Val Lys Ser Lys Phe Asp Ser Leu Asp Phe Asp Thr
165 170 175

45 Leu Leu Lys Gln Ala Gln Lys Asn Leu Arg Arg
180 185

50 (2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Lys Leu Pro Gly Lys Phe Arg Arg Ala His Gln Gly Asn Leu Glu
1 5 10 15

60

Ser Gln Leu Thr Ser Glu Ser Tyr Tyr Lys Glu Thr Leu Ser Val Pro
 20 25 30
 5 Thr Val Glu His Ile Ile Gln Glu Leu Lys Asp Ile Phe Ser Glu Gln
 35 40 45
 His Leu Lys Ala Leu Lys Cys Leu Ser Leu Val Pro Ser Val Met Gly
 50 55 60
 10 Gln Leu Lys Phe Asn Thr Ser Glu Glu His His Ala Asp Met Tyr Arg
 65 70 75 80
 Ser Asp Leu Pro Asn Pro Asp Thr Leu Ser Ala Glu Leu His Cys Trp
 85 90 95
 15 Arg Ile Lys Trp Lys His Arg Gly Lys Asp Ile Glu Leu Pro Ser Thr
 100 105 110
 20 Ile Tyr Glu Ala Leu His Leu Pro Asp Ile Lys Phe Phe Pro Asn Val
 115 120 125
 Tyr Ala Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu
 130 135 140
 25 Asn Glu Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg
 145 150 155 160
 Asn Thr Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile
 165 170 175
 30 Asn Phe Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile
 180 185 190
 35 Lys Leu Tyr Thr Xaa Xaa Ser Xaa Leu Xaa Thr Xaa Xaa Ser Xaa Xaa
 195 200 205
 Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
 210 215 220
 40 Asp Xaa Xaa Xaa Arg Glu Lys Ala Val Arg Cys Met Xaa
 225 230 235
 45 (2) INFORMATION FOR SEQ ID NO: 412:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:
 Met Lys Pro Met Ala Val Val Ala Ser Thr Val Leu Gly Leu Val Gln
 1 5 10 15
 55 Asn Met Arg Ala Phe Gly Gly Ile Leu Val Val Val Tyr Tyr Val Phe
 20 25 30
 60 Ala Ile Ile Gly Ile Asn Leu Phe Arg Gly Val Ile Val Ala Leu Pro
 35 40 45

Gly Asn Ser Ser Leu Ala Pro Ala Asn Gly Ser Ala Pro Cys Gly Ser
 50 55 60
 5 Phe Glu Gln Leu Glu Tyr Trp Ala Asn Asn Phe Asp Asp Phe Ala Ala
 65 70 75 80
 Ala Leu Val Thr Leu Trp Asn Leu Met Val Val Asn Asn Trp Gln Val
 85 90 95
 10 Phe Leu Asp Ala Tyr Arg Arg Tyr Ser Gly Pro Trp Ser Lys Ile Tyr
 100 105 110
 15 Phe Val Leu Trp Trp Leu Val Ser Ser Val Ile Trp Val Asn Leu Phe
 115 120 125
 Leu Ala Leu Ile Leu Glu Asn Phe Leu His Lys Trp Asp Pro Arg Ser
 130 135 140
 20 His Leu Gln Pro Leu Ala Gly Thr Pro Glu Ala Thr Tyr Gln Met Thr
 145 150 155 160
 Val Glu Leu Leu Phe Arg Asp Ile Leu Glu Glu Pro Gly Glu Asp Glu
 165 170 175
 25 Leu Thr Glu Arg Leu Ser Gln His Pro His Leu Trp Leu Cys Arg Xaa
 180 185 190

30

- 35 (2) INFORMATION FOR SEQ ID NO: 413:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Asn Val Val Val Val Ala Phe Gly Leu Ile Leu Ile Ile Glu Ser Leu
 1 5 10 15
 45 Gly Glu Gln Cys Pro
 20

- 50 (2) INFORMATION FOR SEQ ID NO: 414:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys
 1 5 10 15
 60

Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala
 20 25 30
 Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg
 5 35 40 45
 Ala Pro Xaa
 50

10

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

20 Met Leu Ile Ile Ser Leu Arg Pro Gln Phe Pro Ser Leu Ile Val Gln
 1 5 10 15
 Leu Glu Cys Ser Val Leu Phe Leu Pro Ile Ser Leu Asn Leu Leu Leu
 20 25 30
 25

30

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
 1 5 10 15
 Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
 20 25 30
 45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
 35 40 45
 Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
 50 55 60
 Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
 65 70 75 80
 55 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
 85 90 95
 Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
 100 105 110
 60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

115 120 125

Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg
 130 135 140

5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Ile Gly Arg Pro
 145 150 155 160

10 Gln Val Xaa

(2) INFORMATION FOR SEQ ID NO: 417:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
 1 5 10 15

25 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
 20 25 30

Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
 35 40 45

30 Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
 50 55 60

35 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser
 65 70 75 80

Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln
 85 90 95

40 Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val
 100 105 110

Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu
 115 120 125

45 Ala Pro Gly Arg Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro
 130 135 140

50 Trp Phe Thr Ala Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys
 145 150 155 160

Arg Gln Arg Arg Gln Glu Arg Arg Gln Met Lys Arg Leu Xaa
 165 170

55

(2) INFORMATION FOR SEQ ID NO: 418:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

5 Met Glu Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Val Ala Met Met
 1 5 10 15

Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala Leu Arg
 20 25 30

10 Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Cys Cys Leu
 35 40 45

15 Ala Xaa
 50

(2) INFORMATION FOR SEQ ID NO: 419:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Leu Gly Lys Gly Gly Gly Arg Ala Gly Leu Leu Arg Tyr Arg Leu
 1 5 10 15

30 Leu Tyr Phe Thr Leu Val Val Gly Glu Gly Glu Pro Gly Glu Asn Lys
 20 25 30

Val Thr Ile Pro Phe Phe Glu Thr Gly Lys Lys Ile Ile Phe Cys Ser
 35 40 45

35 Val Lys Met Val Glu Asn Ser Asn Val Pro Ser His Lys Gly Pro Val
 50 55 60

40 Pro Leu Arg Ser Glu Gln Trp Glu Leu Lys Ile Ser Glu Thr Leu Gly
 65 70 75 80

Glu Gly Lys Ile Gly Phe Leu Leu Ile Gly Arg Cys Ser Ser Gly Xaa
 85 90 95

45 Gly Gly Leu Cys Phe Cys Trp Asp Val Leu Cys Cys Met Tyr Ala Tyr
 100 105 110

Met Asp Arg Ser Leu Leu Ser Leu
 115 120

50

(2) INFORMATION FOR SEQ ID NO: 420:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

606

Met Thr His Leu Leu Leu Thr Ala Thr Val Thr Pro Ser Glu Gln Asn
 1 5 10 15

5 Ser Ser Arg Glu Pro Gly Trp Glu Thr Ala Met Ala Lys Asp Ile Leu
 20 25 30

Gly Glu Ala Gly Leu His Phe Asp Glu Leu Asn Lys Leu Arg Val Leu
 35 40 45

10 Asp Pro Glu Val Thr Gln Gln Thr Ile Glu Leu Lys Glu Glu Cys Lys
 50 55 60

Asp Phe Val Asp Lys Ile Gly Gln Phe Gln Lys Ile Val Gly Gly Leu
 65 70 75 80

15 Ile Glu Leu Val Asp Gln Leu Ala Lys Glu Ala Glu Asn Glu Lys Met
 85 90 95

Lys Ala Ile Gly Ala Arg Asn Leu Leu Lys Ser Ile Ala Lys Gln Arg
 100 105 110

Glu Ala Gln Gln Gln Gln Leu Gln Ala Leu Ile Ala Glu Lys Lys Met
 115 120 125

25 Gln Leu Glu Arg Tyr Arg Val Glu Tyr Glu Ala Leu Cys Lys Val Glu
 130 135 140

Ala Glu Gln Asn Glu Phe Ile Asp Gln Phe Ile Phe Gln Lys Xaa
 145 150 155

30

(2) INFORMATION FOR SEQ ID NO: 421:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

40 Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
 1 5 10 15

45 Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 20 25 30

Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 35 40 45

50 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 50 55 60

His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80

55 Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
 85 90 95

60 Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
 100 105 110

Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
 115 120 125

5 Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
 130 135 140

Val Arg Ile Phe Gly Ile Asn Lys Tyr Xaa
 145 150

10

(2) INFORMATION FOR SEQ ID NO: 422:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

20 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala Leu
 1 5 10 15

25 Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Ile Gly Ile Ala Ala
 20 25 30

Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val Val Gly Val
 35 40 45

30 Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala Leu Val Gly Leu
 50 55 60

Ile Gly Ala Val Lys His His Gln Val Leu Leu Phe Phe Tyr Met Ile
 65 70 75 80

35 Ile Leu Leu Leu Val Phe Ile Val Gln Phe Ser Val Ser Cys Ala Cys
 85 90 95

40 Leu Ala Leu Asn Gln Glu Gln Gln Gly Gln Leu Leu Glu Val Gly Trp
 100 105 110

Asn Asn Thr Ala Ser Ala Arg Asn Asp Ile Gln Arg Asn Leu Asn Cys
 115 120 125

45 Cys Gly Phe Arg Ser Val Asn Pro Asn Asp Thr Cys Leu Ala Ser Cys
 130 135 140

Val Lys Ser Asp His Ser Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu
 145 150 155 160

50 Tyr Ala Gly Glu Val Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe
 165 170 175

Ser Phe Thr Glu Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn
 180 185 190

Gln Lys Asp Pro Arg Ala Asn Pro Ser Ala Phe Leu
 195 200

60

(2) INFORMATION FOR SEQ ID NO: 423:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

10 Met Leu Gln Ser Ile Ile Lys Asn Ile Trp Ile Pro Met Lys Pro Tyr
 1 5 10 15

Tyr Thr Lys Val Tyr Gln Glu Ile Trp Ile Gly Met Gly Leu Met Gly
 20 25 30

15 Phe Ile Val Tyr Lys Ile Arg Ala Ala Asp Lys Arg Ser Lys Ala Leu
 35 40 45

Lys Ala Ser Ala Pro Ala Pro Gly His His Asn Gln Ile Tyr Leu Glu
 20 50 55 60

Tyr Met Xaa
 65

25

(2) INFORMATION FOR SEQ ID NO: 424:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

35 Met Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val
 1 5 10 15

Ala Val Asn Asn Pro Lys Lys Gln Glu
 20 25

40

(2) INFORMATION FOR SEQ ID NO: 425:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

50

Met Ala Ala Xaa Glu Pro Ala Val Leu Ala Leu Pro Asn Ser Gly Ala
 1 5 10 15

55 Gly Gly Ala Gly Ala Pro Ser Gly Thr Val Pro Val Leu Phe Cys Phe
 20 25 30

Ser Val Phe Ala Arg Pro Ser Ser Val Pro His Gly Ala Gly Tyr Glu
 35 40 45

60 Leu Leu Ile Gln Lys Phe Leu Ser Leu Tyr Gly Asp Gln Ile Asp Met

50 55 60
 His Arg Lys Phe Val Val Gln Leu Phe Ala Glu Glu Trp Gly Gln Tyr
 65 70 75 80
 5 Val Asp Leu Pro Lys Gly Phe Ala Val Ser Glu Arg Cys Lys Val Arg
 85 90 95
 10 Leu Val Pro Leu Gln Ile Gln Leu Thr Thr Leu Gly Asn Leu Thr Pro
 100 105 110
 Ser Ser Thr Val Phe Phe Cys Cys Asp Met Gln Glu Arg Phe Arg Pro
 115 120 125
 15 Ala Ile Lys Tyr Phe Gly Asp Ile Ile Ser Val Gly Gln Arg Leu Leu
 130 135 140
 Gln Gly Ala Arg Ile Leu Gly Ile Pro Val Ile Val Thr Glu Gln Tyr
 20 145 150 155 160
 Pro Lys Gly Leu Gly Ser Thr Val Gln Glu Ile Asp Leu Thr Gly Val
 165 170 175
 25 Lys Leu Val Leu Pro Lys Thr Lys Phe Ser Met Val Leu Pro Glu Val
 180 185 190
 Glu Ala Ala Leu Ala Glu Ile Pro Gly Val Arg Ser Val Val Leu Phe
 195 200 205
 30 Gly Val Glu Thr His Val Cys Ile Gln Gln Thr Ala Leu Glu Leu Val
 210 215 220
 Gly Arg Gly Val Glu Val His Ile Val Ala Asp Ala Thr Ser Ser Arg
 35 225 230 235 240
 Ser Met Met Asp Arg Met Phe Ala Leu Glu Arg Leu Ala Xaa Xaa Gly
 245 250 255
 40 Ile Ile Val Thr Thr Ser Glu Ala Val Leu Leu Gln Leu Val Ala Asp
 260 265 270
 Lys Asp His Pro Lys Phe Lys Glu Ile Gln Asn Leu Ile Lys Ala Ser
 275 280 285
 45 Ala Pro Glu Ser Gly Leu Leu Ser Lys Val Xaa
 290 295

50 (2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Arg Asp Leu Gly Thr Leu Leu Ser Pro Val Cys Ser
 1 5 10

60

(2) INFORMATION FOR SEQ ID NO: 427:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

10

Met Phe Gly Cys Leu Val Ala Gly Arg Leu Val Gln Thr Ala Ala Gln
 1 5 10 15

15

Gln Val Ala Glu Asp Lys Phe Val Phe Asp Leu Pro Asp Tyr Glu Ser
 20 25 30

Ile Asn His Val Val Val Phe Met Leu Gly Thr Ile Pro Phe Pro Glu
 35 40 45

20

Gly Met Gly Gly Ser Val Tyr Phe Ser Tyr Pro Asp Ser Asn Gly Met
 50 55 60

Pro Val Trp Gln Leu Leu Gly Phe Val Thr Asn Gly Lys Pro Ser Ala
 65 70 75 80

25

Ile Phe Lys Ile Ser Gly Leu Lys Ser Gly Glu Gly Ser Gln His Pro
 85 90 95

30

Phe Gly Ala Met Asn Ile Val Arg Thr Pro Ser Val Ala Gln Ile Gly
 100 105 110

Ile Ser Val Glu Leu Leu Asp Ser Met Ala Gln Gln Thr Pro Val Gly
 115 120 125

35

Asn Ala Ala Val Ser Ser Val Asp Ser Phe Thr Gln Phe Thr Gln Lys
 130 135 140

Met Leu Asp Asn Phe Tyr Asn Phe Ala Ser Ser Phe Ala Val Ser Gln
 145 150 155 160

40

Ala Gln Met Thr Pro Ser Pro Ser Glu Met Phe Ile Pro Ala Asn Val
 165 170 175

45

Val Leu Lys Trp Tyr Glu Asn Phe Gln Arg Arg Leu Ala Gln Asn Pro
 180 185 190

Xaa Phe Trp Xaa Thr Xaa
 195

50

(2) INFORMATION FOR SEQ ID NO: 428:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

60

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser

1 5 10 15

Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Leu Trp Lys
20 25 30

5

Asn Arg Gly Gly Val Gly Arg Ser Val Met Ser Ala Val Glu Xaa
35 40 45

10

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

15

20 Met Lys Lys Val Glu Glu Lys Arg Val Asp Val Asn Ser Ala Val Ala
1 5 10 15

Met Gly Glu Val Ile Leu Ala Val Cys His Pro Asp Cys Ile Thr Thr
20 25 30

25 Ile Lys His Trp Ile Thr Ile Ile Arg Ala Arg Phe Glu Glu Val Leu
35 40 45

Thr Trp Ala Lys Gln His Gln Gln Arg Leu Glu Thr Ala Leu Ser Glu
50 55 60

30 Leu Val Ala Asn Ala Glu Leu Leu Glu Glu Leu Leu Ala Trp Ile Gln
65 70 75 80

35 Trp Ala Glu Thr Thr Leu Ile Gln Arg Asp Gln Glu Pro Ile Pro Gln
85 90 95

Asn Ile Asp Arg Val Lys Ala Leu Ile Ala Glu His Gln Thr Phe Met
100 105 110

40 Glu Glu Met Thr Arg Lys Gln Pro Asp Val Asp Arg Val Thr Lys Thr
115 120 125

Tyr Lys Arg Lys Asn Ile Glu Pro Thr His Ala Pro Phe Ile Glu Lys
130 135 140

45 Ser Arg Ser Gly Gly Arg Lys Ser Leu Ser Gln Pro Thr Pro Pro Pro
145 150 155 160

Met Pro Ile Leu Ser Gln Ser Glu Ala Lys Asn Pro Arg Ile Asn Gln
165 170 175

Leu Ser Ala Arg Trp Gln Gln Val Trp Leu Leu Ala Leu Glu Arg Gln
180 185 190

55 Arg Lys Leu Asn Asp Ala Leu Asp Arg Leu Glu Glu Leu Lys Glu Phe
195 200 205

Ala Asn Phe Asp Phe Asp Val Trp Arg Lys Lys Tyr Met Arg Trp Met
210 215 220

60

Asn His Lys Lys Ser Arg Val Met Asp Phe Phe Arg Arg Ile Asp Lys
 225 230 235 240
 5 Asp Gln Asp Gly Lys Ile Thr Arg Gln Glu Phe Ile Asp Gly Ile Leu
 245 250 255
 Ala Ser Lys Phe Pro Thr Thr Lys Leu Glu Met Thr Ala Val Ala Asp
 260 265 270
 10 Ile Phe Asp Arg Asp Gly Asp Gly Tyr Ile Asp Tyr Tyr Glu Phe Val
 275 280 285
 Ala Ala Leu His Pro Asn Lys Asp Ala Tyr Arg Pro Thr Thr Asp Ala
 290 295 300
 15 Asp Lys Ile Glu Asp Glu Val Thr Arg Gln Val Ala Gln Cys Lys Cys
 305 310 315 320
 20 Ala Lys Arg Phe Gln Val Glu Gln Ile Gly Glu Asn Lys Tyr Arg Phe
 325 330 335
 Phe Leu Gly Asn Gln Phe Gly Asp Ser Gln Gln Leu Arg Leu Val Arg
 340 345 350
 25 Ile Leu Arg Asn Arg Asp Gly Ser Arg Trp Trp Arg Met Asp Gly Leu
 355 360 365
 Gly Xaa
 370
 30
 (2) INFORMATION FOR SEQ ID NO: 430:
 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:
 40 Met Asn Val Lys Thr Phe Ser Xaa Asp His Met His Phe Leu Cys Cys
 1 5 10 15
 45 Leu Tyr Leu Arg Tyr Val Thr Phe Val Tyr Leu Asn Leu Phe
 20 25 30
 (2) INFORMATION FOR SEQ ID NO: 431:
 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:
 Met Glu Pro His Leu Arg Cys Arg Val Thr Arg Val Arg Gly Ser Leu
 1 5 10 15
 60 Gly Asn Thr Gly Arg Trp Leu Leu

20

5 (2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met His Tyr Leu Val Leu Gly Gly Leu Gly Val Phe Leu Phe Phe Ser
 1 5 10 15
 Cys Phe Val Phe Leu Phe Phe Xaa Phe Ser Phe Ala Phe Phe Pro Phe
 20 25 30
 Tyr Leu Glu Gly Met Gly Gly Ser Gly Asn Arg Glu Val Gly Gly Gly
 35 40 45
 Phe Cys Leu Phe Phe
 50

25

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Val Ser Lys Ala Leu Leu Arg Leu Val Ser Ala Val Asn Arg Arg
 1 5 10 15
 Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser
 20 25 30
 Val Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu
 35 40 45
 Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu
 50 55 60
 Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val
 65 70 75 80
 Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Ile Thr Gly Gly
 85 90 95
 Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys Leu Met Met Asp Gly
 100 105 110
 His Glu Val Thr Val Val Asp Asn Phe Phe Thr Gly Arg Lys Arg Asn
 115 120 125
 Val Glu His Trp Ile Gly His Glu Asn Phe Glu Leu Ile Asn His Asp
 130 135 140

60

Val Trp Ser Pro Ser Thr Ser Arg Leu Thr Arg Tyr Thr Ile Trp His
 145 150 155 160

5 Leu Gln Pro Pro Leu Gln Thr Thr Cys Ile Ile Leu Ser Arg His Xaa
 165 170 175

10

(2) INFORMATION FOR SEQ ID NO: 434:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

20

Met Leu Arg Cys Trp Pro Leu Phe Trp Leu Pro Leu Val Ser Pro Phe
 1 5 10 15

25 Cys Ser Leu Phe Trp Leu Leu Val Glu Trp Phe Gly Thr Asn Ile Asp
 20 25 30

Arg Glu Ser Tyr Asp Ala Ile Gly Gly Pro Ser Trp Met Thr Ala Ser
 35 40 45

30 Ser Phe Cys Leu Ser Asn Ser Asn Ile Trp Ser Leu Glu Ile Ser Ser
 50 55 60

35 Gly Ser Thr Ser Val Val His Ser Gln Gln Ala Met Asp
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 435:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

45

Met Arg Ser Cys Glu Ile Gln Leu Cys Val Trp Leu Leu Val Ser Ser
 1 5 10 15

50 His Val Asp Met Val Leu Gly Gly Ser Pro Ser Thr Leu Tyr Met Met
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 436:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

5 Met Val Val Asn Ser Leu Cys Phe Leu Ser Leu Leu Leu Val Ile Leu
 1 5 10 15
 Glu Leu Ser Thr Asp Ser Ser Ala Arg Leu Leu Tyr His Glu
 20 25 30
 10

(2) INFORMATION FOR SEQ ID NO: 437:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

20 Met Asp Lys Gln Lys His Leu Glu Val Arg Arg Ser Val Phe Lys Ile
 1 5 10 15
 25 Gln Gly Lys Ile Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser
 20 25 30
 Pro Thr Ile Phe Ser His Ser Ile Leu Leu Leu Leu Pro His His Val
 35 40 45
 30 Leu Pro Cys Thr Pro Gln Met Val Arg Gly Val Thr Gln Val Leu Arg
 50 55 60
 Glu Phe Gly Asp Gln
 65
 35

(2) INFORMATION FOR SEQ ID NO: 438:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

45 Met Pro Leu Cys Phe Phe Ser Phe Leu Cys Cys Trp Val Leu Val Phe
 1 5 10 15
 50 Lys Leu Ile

(2) INFORMATION FOR SEQ ID NO: 439:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg
 1 5 10 15
 5 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg
 20 25 30
 Arg Val Met Val Asn Leu Asn Ile Leu Phe Xaa
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 440:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

20

Met Leu Leu Phe Pro Ser Leu Leu Phe Ala Ala Thr Tyr Asn Val Ala
 1 5 10 15
 25 Asn Pro Ser Arg Leu Ile Leu Tyr Met Ile Ser Ala Gly Ala Asp Ser
 20 25 30

Gln

30

(2) INFORMATION FOR SEQ ID NO: 441:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

40 Met Trp Gln Val Arg Gly Leu Pro Pro Val Pro Leu Leu Leu Thr Met
 1 5 10 15
 Ser Pro Pro Pro Cys Leu Ser Ser Pro Phe Pro Phe Ile Ser Val Pro
 20 25 30
 45 Leu Phe Glu Ala Val Pro Ile Ser Val Ser Asp Gln Pro Ser Pro Xaa
 35 40 45

50 Leu Thr Thr Leu Leu
 50

(2) INFORMATION FOR SEQ ID NO: 442:

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Ile Thr Ser Val Leu Val Phe Leu Ile Phe Phe Phe Pro Tyr Leu
 1 5 10 15
 5 Ser Leu Val Thr Leu Leu Gln Ala Arg Asn Leu Trp Val Ile His Arg
 20 25 30
 Ala Ala Leu Cys Glu Ser Gly Leu Phe His Trp Arg Lys Gly Ile Glu
 35 40 45
 10 Asn Gln Leu Glu Pro Met Tyr Phe Leu Pro His Gly Thr Leu Phe Leu
 50 55 60

15

- (2) INFORMATION FOR SEQ ID NO: 443:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Leu Tyr Ser Cys Glu Pro Tyr Leu Ile Ile Leu Asn Ile Tyr Ser
 1 5 10 15
 30 Gln Lys Ala Phe Tyr Phe Tyr Phe Phe Glu Gly Ser Phe Ser Val Cys
 20 25 30
 Thr Leu

35

- (2) INFORMATION FOR SEQ ID NO: 444:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Arg Gln Arg Gln Ala Ala Cys Gln Pro Pro Pro Ser Arg Asn Gly
 1 5 10 15
 50 Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val
 20 25 30
 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Ser Ser Pro Leu
 35 40 45
 55 Asn Leu Leu Leu Val Ser Ile Ser Trp Asp Leu Gly Leu Lys Leu
 50 55 60
 Asn Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr
 65 70 75 80

60

Lys Lys Phe Asn Lys Lys Lys Lys Lys
85

5

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

15 Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

20 Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
25 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

30 Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

35 Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
40 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

45 Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

50 Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
55 210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

60 Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
 260 265 270

5 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
 275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Pro Pro Gly Pro Glu Lys Ser
 290 295 300

10 Gly Asn Pro Arg Thr Pro Ser Thr Leu Thr Ser Gln Gly Gln Gly Arg
 305 310 315 320

Glu Ala Ala Leu Leu Gly Leu Leu Thr Leu Gln Gly Thr Val Ala Phe
 15 325 330 335

Val Glu Thr Leu Met Glu Ile Cys Leu Thr Ser Gly Lys Asp
 340 345 350

20

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

30 Met Val Phe Leu Pro Arg Gly Val Val Val Ser Gly Gly Ala Ala Cys
 1 5 10 15

Leu Trp Leu Thr Phe Ile Leu Glu Thr Glu Val Tyr Leu Asp Leu Ala
 20 25 30

35 Thr Glu Ala Arg Ala His Ser Arg Met Gly Leu Gly Leu Trp Pro Pro
 35 40 45

Asn

40

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Ser Ala Glu Leu Asp Tyr Thr Ile Glu Ile Pro Asp Gln Pro
 1 5 10 15

55 Cys Trp Ser Gln Lys Asn Ser Pro Ser Pro Gly Gly Lys Glu Ala Glu
 20 25 30

Thr Arg Gln Pro Val Val Ile Leu Leu Gly Trp Gly Gly Cys Lys Asp
 35 40 45

60

620

Lys Asn Leu Ala Lys Tyr Ser Ala Ile Tyr His Lys Arg Gly Cys Ile
 50 55 60
 Val Ile Arg Tyr Thr Ala Pro Trp His Met Val Phe Phe Ser Glu Ser
 5 65 70 75 80
 Leu Gly Ile Pro Ser Leu Arg Val Leu Ala Gln Lys Leu Leu Glu Leu
 85 90 95
 10 Leu Phe Asp Tyr Glu Ile Glu Lys Glu Pro Leu Leu Phe His Val Phe
 100 105 110
 Ser Asn Gly Gly Val Met Leu Tyr Arg Tyr Val Leu Glu Leu Leu Gln
 115 120 125
 15 Thr Arg Arg Phe Cys Arg Leu Arg Val Val Gly Thr Ile Phe Asp Ser
 130 135 140
 Ala Pro Gly Asp Ser Asn Leu Val Gly Ala Leu Arg Ala Leu Ala Ala
 145 150 155 160
 Ile Leu Glu Arg Arg Ala Ala Met Leu Arg Leu Leu Leu Val Ala
 165 170 175
 25 Phe Ala Leu Val Val Val Leu Phe His Val Leu Leu Ala Pro Ile Thr
 180 185 190
 Ala Xaa Phe His Thr His Phe Tyr Asp Arg Leu Gln Asp Ala Gly Ser
 195 200 205
 30 Arg Trp Pro Glu Leu Tyr Leu Tyr Ser Arg Ala Asp Glu Val Val Leu
 210 215 220
 Ala Arg Asp Ile Glu Arg Met Val Glu Ala Arg Leu Ala Arg Arg Val
 225 230 235 240
 Leu Ala Arg Ser Val Asp Phe Val Ser Ser Ala His Val Ser His Leu
 245 250 255
 40 Arg Asp Tyr Pro Thr Tyr Tyr Thr Ser Leu Cys Val Asp Phe Met Arg
 260 265 270
 Asn Cys Val Arg Cys Xaa
 275

45

(2) INFORMATION FOR SEQ ID NO: 448:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

55

Met Ser Phe Ile Phe Asp Trp Ile Tyr Ser Gly Phe Ser Ser Val Leu
 1 5 10 15

60

Gln Phe Leu Gly Leu Tyr Lys Lys Thr Gly Lys Leu Val Phe Leu Gly
 20 25 30

Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
 35 40 45
 5 Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
 50 55 60
 Thr Ile Ala Gly Met Thr Phe Thr Thr Phe Asp Leu Gly Gly His Val
 65 70 75 80
 10 Gln Ala Arg Arg Val Trp Lys Asn Tyr Leu Pro Ala Ile Asn Gly Ile
 85 90 95
 Val Phe Leu Val Asp Cys Ala Asp His Glu Arg Leu Leu Glu Ser Lys
 100 105 110
 15 Glu Glu Leu Asp Ser Leu Met Thr Asp Glu Thr Ile Ala Asn Val Pro
 115 120 125
 20 Ile Leu Ile Leu Gly Asn Lys Ile Asp Arg Pro Glu Ala Ile Ser Glu
 130 135 140
 Glu Arg Leu Arg Glu Met Phe Gly Leu Tyr Gly Gln Thr Thr Gly Lys
 145 150 155 160
 25 Gly Ser Ile Ser Leu Lys Glu Leu Asn Ala Arg Pro Leu Glu Val Phe
 165 170 175
 Met Cys Ser Val Leu Lys Arg Gln Gly Tyr Gly Glu Gly Phe Arg Trp
 180 185 190
 30 Met Ala Gln Tyr Ile Asp Xaa
 195

35

(2) INFORMATION FOR SEQ ID NO: 449:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

45 Met Thr Leu Ser Arg Phe Ala Tyr Asn Gly Lys Arg Cys Pro Ser Ser
 1 5 10 15
 Tyr Asn Ile Leu Asp Asn Ser Lys Ile Ile Ser Glu Glu Cys Arg Lys
 20 25 30
 50 Glu Leu Thr Ala Leu Leu His His Tyr Tyr Pro Ile Glu Ile Asp Pro
 35 40 45
 His Arg Thr Val Lys Glu Lys Leu Pro His Met Val Glu Trp Trp Thr
 50 55 60
 Lys Ala His Asn Leu Leu Cys Gln Gln Lys Ile Gln Lys Phe Gln Ile
 65 70 75 80
 60 Ala Gln Val Val Arg Glu Ser Asn Ala Met Leu Arg Glu Gly Tyr Lys

85 90 95

Thr Phe Phe Asn Thr Leu Tyr His Asn Asn Ile Pro Leu Phe Ile Phe
100 105 110

5 Ser Ala Gly Ile Gly Asp Ile Leu Glu Glu Ile Ile Arg Gln Met Lys
115 120 125

Val Phe His Pro Asn Ile His Ile Val Ser Asn Tyr Met Asp Phe Asn
10 130 135 140

Glu Asp Gly Phe Leu Gln Gly Phe Lys Gly Gln Leu Ile His Thr Tyr
145 150 155 160

15 Asn Lys Asn Ser Ser Val Cys Glu Asn Xaa Gly Tyr Phe Gln Gln Leu
165 170 175

Glu Gly Lys Thr Asn Val Ile Leu Leu Gly Asp Ser Ile Gly Asp Leu
180 185 190

20 Thr Met Ala Asp Gly Val Pro Gly Val Gln Asn Ile Leu Lys Ile Gly
195 200 205

Phe Leu Asn Asp Lys Val Glu Glu Arg Arg Xaa Arg Tyr Met Asp Ser
25 210 215 220

Tyr Asp Ile Val Leu Glu Lys Asp Glu Thr Leu Asp Val Val Asn Gly
225 230 235 240

30 Leu Leu Gln His Ile Leu Cys Gln Gly Val Gln Leu Glu Met Gln Gly
245 250 255

Pro Xaa

35

(2) INFORMATION FOR SEQ ID NO: 450:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Ser His Val Leu Leu Cys Pro Ser Leu Ser Cys Ser Asn Leu Leu
1 5 10 15

50

Pro Pro Ser His Ser Leu Gly Thr Met Gly Ser Leu Ser Pro His Leu
20 25 30

Cys Gly His Thr Met Cys Pro Val Asn Pro Glu Leu Pro Leu Ser Ser
35 40 45

55

Arg Leu Thr Thr Asp Gln Pro Gln Pro Asp Ala Cys Ser Pro Thr Leu
50 55 60

Leu Thr Leu Pro Leu Pro Ser Ser Phe Leu Pro His Ser Lys Pro Thr
65 70 75 80

60

Phe Xaa His Pro Cys Ser Pro
85

5

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

10

15

Met Phe Ser Ile Asn Pro Leu Glu Asn Leu Lys Val Tyr Ile Ser Ser
1 5 10 15

Arg Pro Pro Leu Val Val Phe Met Ile Ser Val Xaa Pro Met Ala Ile
20 25 30

20

Ala Phe Leu Thr Leu Gly Tyr Phe Phe Lys Ile Lys Glu Ile Lys Ser
35 40 45

25

Pro Glu Met Ala Glu Asp Trp Asn Thr Phe Leu Leu Arg Phe Asn Asp
50 55 60

Leu Asp Leu Cys Val Ser Glu Asn Glu Thr Leu Lys His Leu Thr Asn
65 70 75 80

30

Asp Thr Thr Thr Pro Glu Ser Thr Met Thr Ser Gly Gln Ala Arg Ala
85 90 95

Ser Thr Gln Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile
100 105 110

35

Ser Val Ser Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly
115 120 125

Tyr Ser Arg Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln
130 135 140

40

Ile Gly Leu Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe
145 150 155 160

45

Thr Leu Pro Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His
165 170 175

Cys Glu Gln Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro
180 185 190

50

Gly Val Phe Pro Val Thr Val Gln Pro Pro His Cys Val Pro Asp Thr
195 200 205

Tyr Ser Asn Ala Thr Leu Trp Tyr Lys Ile Phe Thr Thr Ala Arg Asp
210 215 220

55

Ala Asn Thr Lys Tyr Ala Gln Asp Tyr Asn Pro Phe Trp Cys Tyr Lys
225 230 235 240

60

Gly Ala Ile Gly Lys Val Tyr His Ala Leu Asn Pro Lys Leu Thr Val
245 250 255

Ile Val Pro Asp Asp Asp Arg Ser Leu Ile Asn Leu His Leu Met His
 260 265 270

5 Thr Ser Tyr Phe Leu Phe Val Met Val Ile Thr Met Phe Cys Tyr Ala
 275 280 285

Val Ile Lys Gly Arg Pro Ser Lys Leu Arg Gln Ser Asn Pro Glu Phe
 290 295 300

10 Cys Pro Glu Lys Val Ala Leu Ala Glu Ala Xaa
 305 310 315

15

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

20 Met Pro Gly Leu Ser Leu Ala Leu Leu Pro Phe Gly Pro Gly Cys Thr
 1 5 10 15

Glu Ala Leu His Ala Gly Cys Phe Pro Ala Phe Ala Ser Ala Thr Arg
 20 25 30

30 Val Asn Gly Glu Ala Ala Leu Ser Pro Gly Leu Cys Asp Pro Ile Ser
 35 40 45

Val Pro Tyr Val
 50

35

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

40

45 Met Ala Val Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys
 1 5 10 15

Gly Phe Ile Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val
 20 25 30

Leu Leu Trp Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala
 35 40 45

55 Gly Leu Lys Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys
 50 55 60

Asp Thr Glu Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys
 65 70 75 80

60

Asp Ser Asn Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala
 85 90 95
 5 Ser Gln Met Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser
 100 105 110
 Tyr Tyr Asn Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu
 115 120 125
 10 Tyr Met Thr Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr
 130 135 140
 Thr Gln Gly Leu Ser Gly Phe His Pro Gln Tyr Phe Asp Gly Ser Ile
 145 150 155 160
 15 Ser Tyr Asn Trp Asn Asn Gly Asn Cys Ser Phe Tyr Leu Ala Thr Ser
 165 170 175
 Lys Met Trp Phe Gly Ser Ala Gly Leu Ile Ser Gly Leu Ala Gln Leu
 180 185 190
 Ser Cys Leu Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro
 195 200 205
 25 Leu Asp Leu Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile
 210 215 220
 Gln Gly Glu Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu
 225 230 235 240
 30 Ile Tyr Met Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr
 245 250 255
 Ser Pro Glu Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly
 260 265 270
 Val Ile Ala Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr
 275 280 285
 40 Gln Leu Leu Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn
 290 295 300
 Gly Val Gln Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile
 305 310 315 320
 45 Met Val Ile Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu
 325 330 335
 Ile Ser Val Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe
 340 345 350
 Ala Gln Asn Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala
 355 360 365
 55 Lys Glu Val Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val Xaa
 370 375 380

60 (2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

5 Met Arg Ser Ile Gly Asn Lys Asn Thr Ile Leu Leu Gly Leu Gly Phe
 1 5 10 15
 10 Gln Ile Leu Gln Leu Ala Trp Tyr Gly Phe Gly Ser Glu Pro Trp Met
 20 25 30
 15 Met Trp Ala Ala Gly Ala Val Ala Ala Met Ser Ser Ile Thr Phe Pro
 35 40 45
 Ala Val Ser Ala Leu Val Ser Arg Thr Ala Asp Ala Asp Gln Gln Gly
 50 55 60
 20 Val Val Gln Gly Met Ile Thr Gly Ile Arg Gly Leu Cys Asn Gly Leu
 65 70 75 80
 Gly Pro Ala Leu Tyr Gly Phe Ile Phe Tyr Ile Phe His Val Glu Leu
 85 90 95
 25 Lys Glu Leu Pro Ile Thr Gly Thr Asp Leu Gly Thr Asn Thr Ser Pro
 100 105 110
 30 Gln His His Phe Glu Gln Asn Ser Ile Ile Pro Gly Pro Pro Phe Leu
 115 120 125
 Phe Gly Ala Cys Ser Val Leu Leu Ala Leu Leu Val Ala Leu Phe Ile
 130 135 140
 35 Pro Glu His Thr Asn Leu Ser Leu Arg Ser Ser Ser Trp Arg Lys His
 145 150 155 160
 Cys Gly Ser His Ser His Pro His Asn Thr Gln Ala Pro Gly Glu Ala
 165 170 175
 40 Lys Glu Pro Leu Leu Gln Asp Thr Asn Val
 180 185

45

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

50 Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
 1 5 10 15
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
 20 25 30
 60 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala

[illegible]

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Arg Ile Gln Val Phe Ile Leu Leu Leu Gly Ala Gly Gly Thr Ser
1 5 10 15

40 Gln Phe Thr Lys Pro Pro Ser Leu Pro Leu Glu Pro Glu Pro Ala Val
 20 25 30

Glu Ser Ser Pro Thr Glu Thr Ser Glu Gln Ile Arg Glu Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO: 457:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Ser Tyr Leu Ala Phe Leu Tyr Met Thr Phe Asp Phe Cys Cys Leu
1 5 10 15

60 Tyr Phe Ser Thr Val Tyr Ala Pro Ser Phe Lys Tyr Ile Cys Val His
20 25 30

Thr Asp Thr His Ile Cys Val Cys Val Cys Ile Tyr Leu Ser Ser Val
 35 40 45

5 Val Ser Lys Ser Ser Ala Glu Ala Asp Gly Val Leu Gln Pro Arg Arg
 50 55 60

His Pro Ala Ser Leu Leu Ile Val Phe Ala Thr Ser Ile Ser Glu Ser
 65 70 75 80

10 Ser Leu Leu Ile Phe Ser Phe Gln Lys Thr Glu Ala Lys Leu Ile Val
 85 90 95

Phe Ala Val Ser Leu Ala Ala Lys Xaa
 100 105

15

(2) INFORMATION FOR SEQ ID NO: 458:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser
 1 5 10 15

30 Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val
 20 25 30

Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro
 35 40 45

35 Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln
 50 55 60

Ala His Thr Val Ala Xaa
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 459:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
 1 5 10 15

55 Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
 20 25 30

Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
 35 40 45

60

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
 50 55 60
 5 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Val Met Gly Pro
 65 70 75 80
 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
 85 90 95
 10 Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
 100 105 110
 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Asn Val Gly
 115 120 125
 15 Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
 130 135 140
 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa
 145 150 155
 20
 25 (2) INFORMATION FOR SEQ ID NO: 460:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:
 Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Ala Pro Ser
 1 5 10 15
 35 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
 20 25 30
 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
 35 40 45
 40 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95
 50 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 55 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160
 60

Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175

5 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190

Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205

10 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220

Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 15 225 230 235 240

Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255

20 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270

Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285

25 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300

Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
 30 305 310 315 320

Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
 325 330

35

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

45

Met Leu Lys Cys Ile
 1 5

50

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ile Leu Thr Leu Leu Ser Val Val Ser Thr Met Ala Ser
 1 5 10

60

(2) INFORMATION FOR SEQ ID NO: 463:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Lys Leu His Pro Pro Pro Pro Ser Pro Val Thr Gln Asp His Arg
1 5 10 15

15

Ser Lys Ser Ser His Ser Asn Trp Met Pro Arg Met Gly Ala Cys Ser
20 25 30

Met Ser Arg Thr Ser Ser Ser Gly Pro Pro Ser Leu Cys Lys Ser Thr
35 40 45

20

Ser Gly Arg Ser Cys Thr Arg Pro His Cys Trp Pro Ser Leu Pro Ala
50 55 60

Trp Val Ser Val Phe Thr Arg Thr Asn Thr Gly Ser Trp Cys Tyr Pro
65 70 75 80

25

Ala Trp Gly Gly Ala Phe Ser Arg Pro Trp Met Ser Ala Gln Ser Met
85 90 95

30

Cys Cys Ala Glu Arg Ser Val Leu Gln Val Ala Cys Arg Leu Leu Asp
100 105 110

Ala Leu Glu Phe Leu His Glu Asn Glu Tyr Val His Gly Asn Val Thr
115 120 125

35

Ala Glu Asn Ile Phe Val Asp Pro Glu Asp Gln Ser Gln Val Thr Leu
130 135 140

Ala Gly Tyr Gly Phe Ala Phe Arg Tyr Cys Pro Ser Gly Lys His Val
145 150 155 160

40

Ala Tyr Val Glu Gly Ser Arg Ser Pro His Glu Gly Asp Leu Glu Phe
165 170 175

45

Ile Ser Met Asp Leu His Lys Gly Cys Gly Pro Ser Arg Arg Xaa Asp
180 185 190

Leu Gln Ser Leu Gly Tyr Cys Met Leu Lys Trp Leu Tyr Gly Phe Leu
195 200 205

50

Pro Trp Thr Asn Cys Leu Pro Xaa Xaa Glu Asp Ile Met Lys Gln Lys
210 215 220

Gln Lys Phe Val Asp Lys Pro Gly Pro Phe Val Gly Pro Cys Gly His
225 230 235 240

55

Trp Ile Arg Pro Ser Glu Thr Leu Gln Lys Tyr Leu Lys Val Val Met
245 250 255

60

Ala Leu Thr Tyr Glu Glu Lys Pro Pro Tyr Ala Met Leu Arg Asn Asn
260 265 270

Leu Glu Ala Leu Leu Gln Asp Leu Arg Val Ser Pro Tyr
 275 280 285

5

(2) INFORMATION FOR SEQ ID NO: 464:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

15 Met Thr Ser Pro Pro Pro His Gln Gly Trp Glu Gln Arg Gly Cys Gly
 1 5 10 15
 Glu Ser Gln Val Pro Leu Ala Leu Ser Arg Val Phe Ser Thr Ser His
 20 25 30
 Tyr Cys Leu Leu Val Ala Asn Gln Ser Ile Phe Phe Pro Cys Leu
 35 40 45
 Trp Ala Val Glu Arg Leu Leu Gly Val Arg Cys Thr Cys Pro Leu Ser
 25 50 55 60
 Trp Gly Lys Arg Ile Ile Ser Glu His Cys Ser Ala Gln Ser Ser Xaa
 65 70 75 80

30

35 (2) INFORMATION FOR SEQ ID NO: 465:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

45 Met His Thr Trp Tyr Asn Asp Arg Arg Gln Asn Cys His Cys Leu Leu
 1 5 10 15
 Phe Phe Leu Ile Tyr Leu Arg Lys Ile Tyr Gln Val Val Pro His Val
 20 25 30
 Pro Leu Leu Val Lys Cys Arg Gly Arg Leu Lys Gly Val Asn Ile
 50 35 40 45

55 (2) INFORMATION FOR SEQ ID NO: 466:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

60

Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val
 1 5 10 15
 5 Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr
 20 25 30
 Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu
 35 40 45
 10 Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser
 50 55 60
 Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu Glu Ala Gln Val Glu
 15 65 70 75 80
 Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro Gln Lys Ala Glu Asn Xaa
 85 90 95
 20
 25 (2) INFORMATION FOR SEQ ID NO: 467:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 30 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:
 Met Ala Ser Gly Ala Asp Ser Lys Gly Asp Asp Leu Ser Thr Ala Ile
 1 5 10 15
 35 Leu Lys Gln Lys Asn Arg Pro Asn Arg Leu Ile Val Asp Glu Ala Ile
 20 25 30
 Asn Glu Asp Asn Ser Val Val Ser Leu Ser Gln Pro Lys Met Asp Glu
 40 35 40 45
 Leu Gln Leu Phe Arg Gly Asp Thr Val Leu Leu Lys Gly Lys Lys Arg
 50 55 60
 45 Arg Glu Ala Val Cys Ile Val Leu Ser Asp Asp Thr Cys Ser Asp Glu
 65 70 75 80
 Lys Ile Arg Met Asn Arg Val Val Arg Asn Asn Leu Arg Val Arg Leu
 50 85 90 95
 Gly Asp Val Ile Ser Ile Gln Pro Cys Pro Asp Val Lys Tyr Gly Lys
 100 105 110
 55 Arg Ile His Val Leu Pro Ile Asp Asp Thr Val Glu Gly Ile Thr Gly
 115 120 125
 Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr Phe Leu Glu Ala Tyr Arg
 130 135 140
 60 Pro Ile Arg Lys Gly Asp Ile Phe Leu Val Arg Gly Gly Met Arg Ala

145 150 155 160
 Val Glu Phe Lys Val Val Glu Thr Asp Pro Ser Pro Tyr Cys Ile Val
 165 170 175
 5 Ala Pro Asp Thr Val Ile His Cys Glu Gly Glu Pro Ile Lys Arg Glu
 180 185 190
 10 Asp Glu Glu Glu Ser Leu Asn Glu Val Gly Tyr Asp Asp Ile Gly Gly
 195 200 205
 Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu Met Val Glu Leu Pro Leu
 210 215 220
 15 Arg His Pro Ala Leu Phe Lys Ala Ile Gly Val Lys Pro Pro Arg Gly
 225 230 235 240
 Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Ile Ala Arg
 245 250 255
 20 Ala Val Ala Asn Glu Thr Gly Ala Phe Phe Phe Leu Ile Asn Gly Pro
 260 265 270
 Glu Ile Met Ser Lys Leu Ala Gly Glu Ser Glu Ser Asn Leu Arg Lys
 25 275 280 285
 Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro Ala Ile Ile Phe Ile Asp
 290 295 300
 30 Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu Lys Thr His Gly Glu Val
 305 310 315 320
 Glu Arg Arg Ile Val Ser Gln Leu Leu Thr Leu Met Asp Gly Leu Lys
 325 330 335
 35 Gln Arg Ala His Val Ile Val Met Ala Ala Thr Asn Arg Pro Asn Ser
 340 345 350
 Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg Phe Asp Arg Glu Val Asp
 40 355 360 365
 Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu Glu Ile Leu Gln Ile His
 370 375 380
 45 Thr Lys Asn Met Lys Leu Ala Asp Asp Val Asp Leu Glu Gln Xaa
 385 390 395

50 (2) INFORMATION FOR SEQ ID NO: 468:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 1 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Leu
1

60

(2) INFORMATION FOR SEQ ID NO: 469:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

10

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
1 5 10 15

15

Pro Pro Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
20 25 30

Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
35 40 45

20

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
50 55 60

25

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
65 70 75 80

Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
85 90 95

30

Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
100 105 110

Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
115 120 125

35

Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
130 135 140

Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
145 150 155 160

40

Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
165 170 175

Ile Val Ile Phe Xaa Ser Lys Pro Arg Asn Pro Arg Tyr Ala Pro His
180 185 190

Leu Glu Pro Gly Ala Leu Pro Asn Leu Xaa Xaa Xaa Ser Leu Ser Lys
195 200 205

50

Met Ser Xaa Xaa Ser Xaa Met Arg Asn Ser Gln Ala His Arg Asn Phe
210 215 220

Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn
225 230 235 240

55

Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu
245 250 255

60

Leu Trp Ile Cys Cys Ala Thr Cys Cys Tyr Thr Leu Leu Asp Ala Val
260 265 270

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 470:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

15 Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe Ser
1 5 10 15
Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr Pro
20 25 30
Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala
35 40 45
25 Thr Glu Lys Arg Leu Thr Lys Leu Leu Val His Ser Ser Leu Val Gly
50 55 60
Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu Ser
65 70 75 80
30 Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu Leu Asp
85 90 95
Lys Asn Asn Ile Pro Thr Arg Ser Tyr Val Ser Tyr Phe Tyr His Asp
100 105 110
35 Ser Leu Tyr Thr Thr Asp Cys Tyr Thr Ala Lys Ala Ser Leu Ala Gly
115 120 125
Xaa Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Leu Ala
40 130 135 140
Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe Pro
145 150 155 160
45 Gly Ser Val Leu Phe Leu Pro His Ser Tyr Ile Gly Asn Ser Gly Met
165 170 175
Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr Ser
180 185 190
50

55

(2) INFORMATION FOR SEQ ID NO: 471:

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

5 Met Arg Lys Thr Arg Leu Trp Gly Leu Leu Trp Met Leu Phe Val Ser
 1 5 10 15
 Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu Leu Lys
 20 25 30
 10 Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu Glu Lys Phe
 35 40 45
 Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro
 50 55 60
 15 Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
 65 70 75 80
 20 Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
 85 90 95
 Arg Val Arg Met Val Asn Leu Gln Val Glu Asp Ser Gly Leu Tyr Gln
 100 105 110
 25 Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
 115 120 125
 Ile Arg Leu Val Val Thr Lys Gly Phe Ser Gly Thr Pro Gly Ser Asn
 130 135 140
 30 Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys
 145 150 155 160
 35 Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro
 165 170 175
 Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu
 180 185 190
 40 Thr Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile
 195 200 205
 Leu Leu Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu
 210 215 220
 45 Phe Ala Val Thr Leu Arg Ser Phe Val Pro
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

60 Met Leu His Ile Leu Pro Leu Lys Ser Tyr Asp Phe Pro His Phe Ser
 1 5 10 15

Leu Met Gly Arg Tyr Arg Cys Ala Ser Leu Leu Phe Cys Phe Leu Leu
 20 25 30
 5 Leu Phe Phe Phe Phe Cys Ser Val Leu Trp Thr Phe Ser Asp Met His
 35 40 45
 Arg Ser Gly Glu Asp Gly Pro Trp Thr Pro Cys Val His His Leu Ala
 50 55 60
 10 Ala Ser Leu Ile Ser Tyr Gly Gln Pro Gly Phe Ile Cys Ile Ser Leu
 65 70 75 80
 Phe Ser Pro Val Leu Phe Ile Glu Asn Pro Arg His Tyr Ala Asn Ala
 85 90 95
 15 Thr Val Thr Thr Leu Gly Asp Trp Xaa
 100 105
 20

(2) INFORMATION FOR SEQ ID NO: 473:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

30 Met Val Phe Leu Lys Tyr Arg Phe Leu Phe Phe Leu Val Phe Leu Ala
 1 5 10 15
 Asn Cys Ile Tyr Ser Leu His Tyr Lys Pro Ser Leu Met Tyr Pro Lys
 20 25 30
 35

40

(2) INFORMATION FOR SEQ ID NO: 474:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

50 Met Ala Leu Ser Arg Gly Leu Pro Arg Glu Leu Ala Glu Ala Val Ala
 1 5 10 15
 Gly Gly Arg Val Leu Val Val Gly Ala Gly Gly Ile Gly Cys Glu Leu
 20 25 30
 55 Leu Lys Asn Leu Val Leu Thr Gly Phe Ser His Ile Asp Leu Ile Asp
 35 40 45
 Leu Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Gln
 50 55 60
 60

Lys Lys His Val Gly Arg Ser Lys Ala Gln Val Ala Lys Glu Ser Val
 65 70 75 80
 5 Leu Gln Phe Tyr Pro Lys Ala Asn Ile Val Ala Tyr His Asp Ser Ile
 85 90 95
 Met Asn Pro Asp Tyr Asn Val Glu Phe Phe Arg Gln Phe Ile Leu Val
 100 105 110
 10 Met Asn Ala Leu Asp Asn Arg Ala Ala Arg Asn His Val Asn Arg Met
 115 120 125
 Cys Leu Ala Ala Asp Val Pro Leu Ile Glu Ser Gly Thr Ala Gly Tyr
 130 135 140
 15 Leu Gly Gln Val Thr Thr Ile Lys Lys Gly Val Thr Glu Cys Tyr Glu
 145 150 155 160
 Cys His Pro Lys Pro Thr Gln Arg Thr Phe Pro Gly Cys Thr Ile Arg
 165 170 175
 20 Asn Thr Pro Ser Glu Pro Ile His Cys Ile Val Trp Ala Lys Tyr Leu
 180 185 190
 25 Phe Asn Gln Leu Phe Gly Glu Glu Asp Ala Asp Gln Glu Val Ser Pro
 195 200 205
 Asp Arg Ala Asp Pro Glu Ala Ala Trp Glu Pro Thr Glu Ala Glu Ala
 210 215 220
 30 Arg Ala Arg Ala Ser Asn Glu Asp Gly Asp Ile Lys Arg Ile Ser Thr
 225 230 235 240
 Lys Glu Trp Ala Lys Ser Thr Gly Tyr Asp Pro Val Lys Leu Phe Thr
 245 250 255
 35 Lys Leu Phe Lys Asp Asp Ile Arg Tyr Leu Leu Thr Met Asp Lys Leu
 260 265 270
 40 Trp Arg Lys Arg Lys Pro Pro Val Pro Leu Asp Trp Ala Glu Val Gln
 275 280 285
 Ser Gln Gly Glu Glu Thr Asn Ala Ser Asp Gln Gln Asn Glu Pro Gln
 290 295 300
 45 Leu Gly Leu Lys Asp Gln Gln Val Leu Asp Val Lys Ser Tyr Ala Arg
 305 310 315 320
 Leu Phe Ser Lys Ser Ile Glu Thr Leu Arg Val His Leu Ala Glu Lys
 325 330 335
 50 Gly Asp Gly Ala Glu Leu Ile Trp Asp Lys Asp Asp Pro Ser Ala Met
 340 345 350
 55 Asp Phe Val Thr Ser Ala Ala Asn Leu Arg Met His Ile Phe Ser Met
 355 360 365
 60 Asn Met Lys Ser Arg Phe Asp Ile Lys Ser Met Ala Gly Asn Ile Ile
 370 375 380

640

Pro Ala Ile Ala Thr Thr Asn Ala Val Ile Ala Gly Leu Ile Val Leu
385 390 395 400

5 Glu Gly Leu Lys Ile Leu Ser Gly Lys Ile Asp Gln Cys Arg Thr Ile
405 410 415

Phe Leu Asn Lys Gln Pro Asn Pro Arg Lys Lys Leu Leu Val Pro Cys
420 425 430

10 Ala Leu Asp Pro Pro Asn Pro Asn Cys Tyr Val Cys Ala Ser Lys Pro
435 440 445

Glu Val Thr Val Arg Leu Asn Val His Lys Val Thr Val Leu Thr Leu
450 455 460

15 Gln Asp Lys Ile Val Lys Glu Lys Phe Ala Met Val Ala Pro Asp Val
465 470 475 480

Gln Ile Glu Asp Gly Lys Gly Thr Ile Leu Ile Ser Ser Glu Glu Gly
20 485 490 495

Glu Thr Glu Ala Asn Asn His Lys Lys Leu Ser Glu Phe Gly Ile Arg
500 505 510

25 Asn Gly Ser Arg Leu Gln Ala Asp Asp Phe Leu Gln Asp Tyr Thr Leu
515 520 525

Leu Ile Asn Ile Leu His Ser Glu Asp Leu Gly Lys Asp Val Glu Phe
30 530 535 540

Glu Val Val Gly Asp Ala Pro Glu Lys Val Gly Xaa Lys Gln Ala Glu
545 550 555 560

35 Asp Ala Ala Lys Ser Ile Thr Asn Gly Gln Xaa
565 570

40 (2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Gln Val Val Thr Cys Leu Thr Arg Asp Ser Tyr Leu Thr His Cys
1 5 10 15

50 Phe Leu Gln His Leu Met Val Val Leu Ser Ser Leu Glu Arg Thr Pro
20 25 30

Ser Pro Glu Pro Val Asp Lys Asp Phe Tyr Ser Glu Phe Gly Asn Lys
35 40 45

55 Thr Thr Gly Lys Met Glu Asn Tyr Glu Leu Ile His Ser Ser Arg Val
50 55 60

60 Lys Phe Thr Tyr Pro Ser Glu Glu Glu Ile Gly Asp Leu Thr Phe Thr
65 70 75 80

Val Ala Gln Lys Met Ala Glu Pro Glu Lys Ala Pro Ala Leu Ser Ile
85 90 95

5 Leu Leu Tyr Val Gln Ala Phe Gln Val Gly Met Pro Pro Pro Gly Cys
100 105 110

Cys Arg Gly Pro Leu Arg Pro Lys Thr Leu Leu Leu Thr Ser Ser Glu
115 120 125

10 Ile Phe Leu Leu Asp Glu Asp Cys Val His Tyr Pro Leu Pro Glu Phe
130 135 140

Ala Lys Glu Pro Pro Gln Arg Asp Arg Tyr Arg Leu Asp Asp Gly Arg
145 150 155 160

Arg Val Arg Asp Leu Asp Arg Val Leu Met Gly Tyr Gln Thr Tyr Pro
165 170 175

20 Gln Pro Ser Pro Ser Ser Ser Met Thr Cys Lys Val Met Thr Ser Trp
180 185 190

Ala Val Ser Pro Trp Thr Thr Leu Gly Arg Cys Gln Val Ala Arg Leu
195 200 205

25 Glu Pro Ala Arg Ala Val Lys Ser Ser Gly Arg Cys Leu Ser Pro Val
210 215 220

Leu Arg Ala Glu Arg Ser Ser Ser Arg Cys Trp Leu Ala Ser Gly Arg
225 230 235 240

Pro Cys Val Ala Val Ser Cys Leu Ser Ser Ser Pro Ala Ser Pro Gly
245 250 255

35 His Ser Gln Pro Val Val Ser Ser Leu Thr Pro Thr Gly Ala Gly Gln
260 265 270

Gln Ala Phe Val Phe Ser Lys Asn Val Leu Ser Ser Leu Trp Tyr Leu
275 280 285

40 Asn Leu Thr Val Leu Ala Glu Asn Val Asn Met Cys Val Cys Cys Val
290 295 300

Asn Ser Phe Ser Cys Trp Glu Xaa
305 310

45

- 50 (2) INFORMATION FOR SEQ ID NO: 476:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Gln His His Leu Trp Ile Leu Leu Leu Cys Leu Gln Thr Trp
1 5 10 15

60 Pro Glu Ala Ala Gly Lys Asp Ser Glu Ile Phe Thr Val Asn Gly Ile

	20	25	30
	Leu Gly Glu Ser Val Thr Phe Pro Val Asn Ile Gln Glu Pro Arg Gln		
	35	40	45
5	Val Lys Ile Ile Ala Trp Thr Ser Lys Thr Ser Val Ala Tyr Val Thr		
	50	55	60
10	Pro Gly Asp Ser Glu Thr Ala Pro Val Val Thr Val Thr His Arg Asn		
	65	70	75
	Tyr Tyr Glu Arg Ile His Ala Leu Gly Pro Asn Tyr Asn Leu Val Ile		
	85	90	95
15	Ser Asp Leu Arg Met Glu Asp Ala Gly Asp Tyr Lys Ala Asp Ile Asn		
	100	105	110
	Thr Gln Ala Asp Pro Tyr Thr Thr Thr Lys Arg Tyr Asn Leu Gln Ile		
	115	120	125
20	Tyr Arg Arg Leu Gly Lys Pro Lys Ile Thr Gln Ser Leu Met Ala Ser		
	130	135	140
25	Val Asn Ser Thr Cys Asn Val Thr Leu Thr Cys Ser Val Glu Lys Glu		
	145	150	155
	Glu Lys Asn Val Thr Tyr Asn Trp Ser Pro Leu Gly Glu Glu Gly Asn		
	165	170	175
30	Val Leu Gln Ile Phe Gln Thr Pro Glu Asp Gln Glu Leu Thr Tyr Thr		
	180	185	190
	Cys Thr Ala Gln Asn Pro Val Ser Asn Asn Ser Asp Ser Ile Ser Ala		
	195	200	205
35	Arg Gln Leu Cys Ala Asp Ile Ala Met Gly Phe Arg Thr His His Thr		
	210	215	220
40	Gly Leu Leu Ser Val Leu Ala Met Phe Phe Leu Leu Val Leu Ile Leu		
	225	230	235
	Ser Ser Val Phe Leu Phe Arg Leu Phe Lys Arg Arg Gln Asp Ala Ala		
	245	250	255
45	Ser Lys Lys Thr Ile Tyr Thr Tyr Ile Met Ala Ser Arg Asn Thr Gln		
	260	265	270
	Pro Ala Glu Ser Arg Ile Tyr Asp Glu Ile Leu Gln Ser Lys Val Leu		
	275	280	285
50	Pro Ser Lys Glu Glu Pro Val Asn Thr Val Tyr Ser Glu Val Gln Phe		
	290	295	300
55	Ala Asp Lys Met Gly Lys Ala Ser Thr Gln Asp Ser Lys Pro Pro Gly		
	305	310	315
	Thr Ser Ser Tyr Glu Ile Val Ile Xaa		
	325		
60			

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

10 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile
 1 5 10 15

Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr
 20 25 30

15 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
 35 40 45

Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
 20 50 55 60

Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
 65 70 75 80

25 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
 85 90 95

Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
 100 105 110

30 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
 115 120 125

Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
 35 130 135 140

Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
 145 150 155 160

40 Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser
 165 170 175

Ala Xaa

45

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

55

Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val
 1 5 10 15

60

Ile Leu Gly Leu Leu Cys Leu Leu Leu Cys Gly Gly Gly Glu Gly Lys
 20 25 30

Val Ala Gly Arg Gln Ala Val Thr Ser Asp Gln Gln Ser Val Gly Arg
 35 40 45

5 Arg Asp Val Tyr
 50

10 (2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Gln Lys Lys Asn Ser Leu Phe Phe Phe Phe Ala Phe Tyr Tyr Glu
 1 5 10 15

20 Asn Lys Thr Asn Ala Pro Gly Glu Gly Ser Met Ile Thr Arg Asn Ile
 20 25 30

25 Lys Glu Tyr Phe Leu Pro Phe Leu Phe Cys Cys Val Glu Ala Ser Ile
 35 40 45

Ala Ile Asn Lys Leu Asn Tyr Leu His Trp Thr His Phe Gln
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

40 Met Pro Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser
 1 5 10 15

45 Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 481:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
 1 5 10 15

60 Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
 20 25 30

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
 35 40 45
 5 His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
 50 55 60
 Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
 65 70 75 80
 10 His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
 85 90 95
 Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
 15 100 105 110
 Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
 115 120 125
 20 Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Xaa Glu Gln
 130 135 140
 Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
 145 150 155 160
 25 Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
 165 170 175
 Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
 30 180 185 190
 Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
 195 200 205
 35 Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
 210 215 220
 Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
 225 230 235 240
 40 Lys Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe
 245 250 255
 Thr Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro
 45 260 265 270
 Val Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe
 275 280 285
 50 Thr Tyr Val Ser Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln
 290 295 300
 Leu Val Pro Glu Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys
 305 310 315 320
 55 Gly Arg Tyr Leu Gln Met Lys Ala Lys Xaa Gln Gly His Ala Xaa Xaa
 325 330 335
 60 Gln Pro Xaa

(2) INFORMATION FOR SEQ ID NO: 482:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Leu Asn Ser Asn Ile Asn Asp Leu Leu Met Val Thr Tyr Leu Ala
1 5 10 15

15

Asn Leu Thr Gln Ser Gln Ile Ala Leu Asn Glu Lys Leu Val Asn Leu
20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 483:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu
1 5 10 15

35

Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr Arg Ile Gly
20 25 30

Cys Phe Lys Thr Ile Thr Cys Trp Pro Thr Ser Leu Thr Gln Arg Xaa
35 40 45

40

45

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Tyr Met Tyr Ser Leu Asn Val Phe Leu Ser Phe Ile Phe Leu Ala
1 5 10 15

55

Leu Val Phe Lys Cys Val His Val Cys Gln Gly Ala Asn Ala Phe Leu
20 25 30

60

Phe Leu Lys Leu Val Phe
35

5 (2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Gly Leu Arg Leu Ile Cys Leu Glu Leu Thr Met Val Lys Ala Leu
 1 5 10 15

15 Val Cys Glu Met Phe Leu Phe Phe Leu Met Thr Gln Lys Leu Ile Trp
 20 25 30

Gln Glu Cys Thr Glu Lys Phe Ala Lys Leu Leu Val Gln Leu Ile Ser
 35 40 45

20 Leu Val Phe Ala Trp Glu Phe Phe Ser Glu Asp Thr Pro
 50 55 60

25 (2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

35 Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
 1 5 10 15

Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
 20 25 30

40 Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys
 35 40 45

Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu
 50 55 60

45 Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met
 65 70 75 80

50 Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu
 85 90 95

Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys
 100 105 110

55 Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr
 115 120 125

60 Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala
 130 135 140

648

Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp
 145 150 155 160
 Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu
 5 165 170 175
 Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala
 180 185 190
 10 Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr
 195 200 205
 Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly
 210 215 220
 15 Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys
 225 230 235 240
 Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe
 20 245 250 255
 Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly
 260 265 270
 25 Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser
 275 280 285
 Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val
 290 295 300
 30 Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu
 305 310 315 320
 Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met
 35 325 330 335
 Leu Ala Thr Gly Gly Asn Arg Lys Lys Xaa
 340 345

40

(2) INFORMATION FOR SEQ ID NO: 487:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

50 Met Glu Glu Val Leu Leu Leu Gly Leu Lys Asp Arg Glu Gly Tyr Thr
 1 5 10 15
 Ser Phe Trp Asn Asp Cys Ile Ser Ser Gly Leu Arg Gly Cys Met Leu
 20 25 30
 55 Ile Glu Leu Ala Leu Arg Gly Arg Leu Gln Leu Glu Ala Cys Gly Met
 35 40 45
 60 Arg Arg Lys Ser Leu Leu Thr Arg Lys Val Ile Cys Lys Ser Asp Ala
 50 55 60

Pro Thr Gly Asp Val Leu Leu Asp Glu Ala Leu Lys His Val Lys Glu
65 70 75 80

5 Thr Gln Pro Pro Glu Thr Val Gln Asn Trp Ile Glu Leu Leu Ser Gly
85 90 95

Glu Thr Trp Asn Pro Leu Lys Leu His Tyr Gln Leu Arg Asn Val Arg
100 105 110

10 Glu Arg Leu Ala Lys Asn Leu Val Glu Lys Gly Val Leu Thr Thr Glu
115 120 125

Lys Gln Asn Phe Leu Leu Phe Asp Met Thr Thr His Pro Leu Thr Asn
130 135 140

Asn Asn Ile Lys Gln Arg Leu Ile Lys Lys Val Gln Glu Ala Val Leu
145 150 155 160

20 Asp Lys Trp Val Asn Asp Pro His Arg Met Asp Arg Arg Leu Leu Ala
165 170 175

Leu Ile Tyr Leu Ala His Ala Ser Asp Val Leu Glu Asn Ala Phe Ala
180 185 190

25 Pro Leu Leu Asp Glu Gln Tyr Asp Leu Ala Thr Lys Arg Val Arg Gln
195 200 205

Leu Leu Asp Leu Asp Pro Glu Val Glu Cys Leu Lys Ala Asn Thr Asn
210 215 220

30 Glu Val Leu Trp Ala Val Val Ala Ala Phe Thr Lys Xaa
225 230 235

35

(2) INFORMATION FOR SEQ ID NO: 488:

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

45 Met Ala Gln Arg Met Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp
1 5 10 15

Ile Glu Lys Asp Gln Ile Ile Glu Met Ala Cys Leu Ile Thr Asp Ser
20 25 30

50 Asp Leu Asn Ile Leu Ala Glu Gly Pro Asn Leu Ile Ile Lys Gln Pro
35 40 45

55 Asp Glu Leu Leu Asp Ser Met Ser Asp Trp Cys Lys Glu His His Gly
50 55 60

Lys Ser Gly Leu Thr Lys Ala Val Lys Glu Ser Thr Ile Thr Leu Gln
65 70 75 80

60 Gln Ala Glu Tyr Glu Phe Leu Ser Phe Val Arg Gln Gln Thr Pro Pro

650

85 90 95

Gly Leu Cys Pro Leu Ala Gly Asn Ser Val His Glu Asp Lys Lys Phe
100 105 110

5 Leu Asp Lys Tyr Met Pro Gln Phe Met Lys His Leu His Tyr Arg Ile
115 120 125

10 Ile Asp Val Ser Thr Val Lys Glu Leu Cys Arg Arg Trp Tyr Pro Glu
130 135 140

Glu Tyr Glu Phe Ala Pro Lys Lys Ala Ala Ser His Arg Ala Leu Asp
145 150 155 160

15 Asp Ile Ser Glu Ser Ile Lys Glu Leu Gln Phe Tyr Arg Asn Asn Ile
165 170 175

Phe Lys Lys Lys Ile Asp Glu Lys Lys Arg Lys Ile Ile Glu Asn Gly
180 185 190

20 Glu Asn Glu Lys Thr Val Ser Xaa
195 200

25

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

35 Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly
1 5 10 15

Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala
20 25 30

40 Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu
35 40 45

Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala
50 55 60

45 Asp Ala Ala Asp Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu
65 70 75 80

50 Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln
85 90 95

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
100 105 110

55 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
115 120 125

Val Arg Thr Gly Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
130 135 140

60

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
 145 150 155 160
 5 Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr
 165 170 175
 Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
 180 185 190
 10 Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
 195 200 205
 Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
 210 215 220
 15 Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
 225 230 235 240
 Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
 245 250 255
 20 Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
 260 265 270
 25 Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
 275 280 285
 Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
 290 295 300
 30 Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
 305 310 315 320
 Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
 325 330 335
 35 Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His Xaa
 340 345 350
 40

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 265 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

50 Met Arg Gly Ser Arg Gly Gly Trp Ala Gly Glu Met Ala Ala Ser Gly
 1 5 10 15
 Glu Ser Gly Thr Ser Gly Gly Gly Gly Ser Thr Glu Glu Ala Phe Met
 20 25 30
 55 Thr Phe Tyr Ser Glu Val Lys Gln Ile Glu Lys Arg Asp Ser Val Leu
 35 40 45
 60 Thr Ser Lys Asn Gln Ile Glu Arg Leu Thr Arg Pro Gly Ser Ser Tyr
 50 55 60

Phe Asn Leu Asn Pro Phe Glu Val Leu Gln Ile Asp Pro Glu Val Thr
 65 70 75 80
 5 Asp Glu Glu Ile Lys Lys Arg Phe Arg Gln Leu Ser Ile Leu Val His
 85 90 95
 Pro Asp Lys Asn Gln Asp Asp Ala Asp Arg Ala Gln Lys Ala Phe Glu
 100 105 110
 10 Ala Val Asp Lys Ala Tyr Lys Leu Leu Leu Asp Gln Glu Gln Lys Lys
 115 120 125
 Arg Ala Leu Asp Val Ile Gln Ala Gly Lys Glu Tyr Val Glu His Thr
 130 135 140
 15 Val Lys Glu Arg Lys Lys Gln Leu Lys Lys Glu Gly Lys Pro Thr Ile
 145 150 155 160
 20 Val Glu Glu Asp Asp Pro Glu Leu Phe Lys Gln Ala Val Tyr Lys Gln
 165 170 175
 Thr Met Lys Leu Phe Ala Glu Leu Glu Ile Lys Arg Lys Glu Arg Glu
 180 185 190
 25 Ala Lys Glu Met His Glu Arg Lys Arg Gln Arg Glu Glu Glu Ile Glu
 195 200 205
 Ala Gln Glu Lys Ala Lys Arg Glu Arg Glu Trp Gln Lys Asn Phe Glu
 210 215 220
 Glu Ser Arg Asp Gly Arg Val Asp Ser Trp Arg Asn Phe Gln Ala Asn
 225 230 235 240
 35 Thr Lys Gly Lys Lys Glu Lys Lys Asn Arg Thr Phe Leu Arg Pro Pro
 245 250 255
 Lys Val Lys Met Glu Gln Arg Glu Xaa
 260 265
 40

(2) INFORMATION FOR SEQ ID NO: 491:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

50 Asp Ser Met Pro Thr Cys Pro Leu Xaa Ala Ser Leu Glu Cys Gly Pro
 1 5 10 15
 Leu Leu Pro Val Arg Leu Cys Cys Leu
 20 25
 55

(2) INFORMATION FOR SEQ ID NO: 492:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Asn Glu Tyr Arg Val Pro Glu Leu Asn Val Gln Asn Gly Val Leu
 1 5 10 15

10 Lys Ser Leu Ser Phe Leu Phe Glu Tyr Ile Gly Glu Met Gly Lys Asp
 20 25 30

Tyr Ile Tyr Ala Val Thr Pro Leu Leu Glu Asp Ala Leu Met Asp Arg
 35 40 45

15 Asp Leu Val His Arg Gln Thr Ala Ser Ala Val Val Gln His Met Ser
 50 55 60

20 Leu Gly Val Tyr Gly Phe Gly Cys Glu Asp Ser Leu Asn His Leu Leu
 65 70 75 80

Asn Tyr Val Trp Pro Asn Val Phe Glu Thr Ser Pro His Val Ile Gln
 85 90 95

25 Ala Val Met Gly Ala Leu Glu Gly Leu Arg Val Ala Ile Gly Pro Cys
 100 105 110

Arg Met Leu Gln Tyr Cys Leu Gln Gly Leu Phe His Pro Ala Arg Lys
 115 120 125

30 Val Arg Asp Val Tyr Trp Lys Ile Tyr Asn Ser Ile Tyr Ile Gly Ser
 130 135 140

35 Gln Asp Ala Leu Ile Ala His Tyr Pro Arg Ile Tyr Gln Arg Xaa
 145 150 155

40 (2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ile Ser Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met
 1 5 10 15

50 Tyr Asp Gly Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln
 20 25 30

Leu Glu Asp Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala
 35 40 45

55 Ala Lys Glu Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu
 50 55 60

60 Phe Ser Gly Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr
 65 70 75 80

Gly Pro Val Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys
 85 90 95
 5 Glu Glu Asn Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro
 100 105 110
 His Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln
 115 120 125
 10 Ala Lys Trp Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys
 130 135 140
 Asn Leu Ile Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro
 15 145 150 155 160
 Thr Leu Lys Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn
 165 170 175
 20 Ser Met Leu Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr
 180 185 190
 Leu Leu Val Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile
 25 195 200 205
 Trp Ile Ser Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln
 210 215 220
 Ala Leu Leu Thr Val Val Ser Gln Val Leu Cys Phe Leu Xaa Ile Glu
 30 225 230 235 240
 Trp Tyr Leu Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn
 245 250 255
 35 Leu Leu Tyr Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val
 260 265 270
 Met Ile Gln Lys Pro Trp Xaa
 275
 40

(2) INFORMATION FOR SEQ ID NO: 494:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:
 Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
 1 5 10 15
 55 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
 20 25 30
 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
 35 40 45
 60 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly

655

50 55 60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Met
65 70 75 80

5 Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe
 85 90 95

10 Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
 100 105 110

Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile
115 120 125

15 Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Xaa Ala
130 135 140

Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145 150 155 160

20 Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
 165 170 175

25 Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
180 185 190

Ala

30

(2) INFORMATION FOR SEQ ID NO: 495:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

40 Met Ala Ala Gly Asp Gln Val Phe Ser Gly Ala Gly His Val Xaa Glu
1 5 10 15

His Val Ala Gly Gly Arg His Ala Trp Leu Leu Thr Trp Gln Ser Ala
20 25 30

45 Cys Pro Ala Asn Arg Leu Ser Leu Val Pro Leu Val Pro Ser Ala Ser
35 40 45

50 Met Thr Arg Leu Met Arg Xaa Arg Thr Ala Ser Gly Ser Ser Val Ile
50 55 60

Leu Trp Met Ala Pro Ala Ala Ala Pro Thr Pro Ala Arg Ala Pro Glu
65 70 75 80

55 Ala Ala Pro Thr Pro Ala Arg Ala Pro Ala Ala Ala Arg Thr Pro Ala
85 90 95

Arg Gly Pro Thr Trp Thr Ser Pro Pro Thr Arg Val Leu Leu Gly Thr
100 105 110

60

656

Xaa Pro Gly Pro Ser Pro Trp Arg Ser Pro Ala Arg Arg Pro Ala Gln
115 120 125

5 Leu Pro Pro Pro Asp Ser Asp Leu Cys Ser Gly Pro Leu Leu Pro Gly
130 135 140

Pro Phe Ser Pro Pro Ala Cys His Thr Ala Pro Asn Ser Val Leu Ile
145 150 155 160

10 Gln Ser Leu Phe Cys Lys Ser Glu Leu Trp Trp Arg Gln Met Arg Ser
165 170 175

Ile Thr Trp Val Pro Ser Pro Lys Ala Gly Trp Arg Trp Thr Lys Gly
180 185 190

15 Arg Lys Gln Ala Ser Pro His Arg Ile Leu Phe His Xaa
195 200 205

20

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

30 Met Ala Leu Thr Leu Leu Pro Ser Val Ser Arg Leu Pro Gly Glu Arg
1 5 10 15

Met Ala Ala Ser Gly Leu Pro Tyr Val Leu His His Lys Ser Ser Leu
20 25 30

35 Met Lys Val Ile Phe Phe Pro Tyr Pro Val Leu Pro Leu Pro Ala Pro
35 40 45

40 Asn Gly Thr Trp Val Pro Arg Leu Val Leu Gly Leu Gly Ser Gly Asp
50 55 60

Gln Val His Tyr Leu Pro Ile Ser Ser Ser Ile Val Asn Tyr Gly Thr
65 70 75 80

45 Ser Val Ser Gly Lys Ser Trp Val Phe Leu Val Tyr Pro Leu His Pro
85 90 95

Thr Pro Thr Trp Ser Thr Arg Cys Phe Gln Val Trp Asp Leu Leu Ser
100 105 110

50 Val Glu Leu Pro Asp Lys Gly Glu Gly Asn Thr Arg Arg Ala Ser Gly
115 120 125

55 Val Pro Gly Leu Ser Gln Leu Pro Thr Ser His Lys Pro Ile Lys Gln
130 135 140

Glu Tyr Xaa
145

60

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

5 Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val
 10 1 5 10 15
 Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys Glu Val Gly
 20 25 30
 15 Ala Ala Leu Pro Pro Arg Gly Pro Ser Leu Ser Asp Cys Leu Gly Leu
 35 40 45
 Pro Pro Trp Thr Pro Trp Gly Pro Ala Trp Thr Leu Ala Gln Ser Xaa
 50 55 60
 20

25

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

30 Met Ser Thr Gly Ala Leu Asn Thr Ser Pro Pro Ala Ser Asn Arg Leu
 35 1 5 10 15
 Glu Ser Thr Leu Asn Glu Tyr Leu Ile Gln Pro Gln Leu His Cys Ser
 20 25 30
 40 Ser Val Gln Arg Leu Thr Leu Lys Trp Gly Cys Ser Ser Leu Gln Arg
 35 40 45
 Asp Gly Gln Ala Val Pro Trp Gly Leu Trp Gln Arg Ala Tyr Pro Ser
 50 55 60
 45 Leu Leu Pro Thr Leu Pro Ser Asp Leu Leu Arg Pro His Ala Val Thr
 65 70 75 80
 50 Pro Ser Val Ser Val Ser Val His Thr Cys Glu Ser Ser Xaa
 85 90

55

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

60

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Xaa Leu Phe Ser Ser Ser
1 5 10 15

5 Leu Pro Phe Leu Trp Leu
20

10 (2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Arg Gly Gly Leu Cys Pro Leu Leu Val Pro Gly Pro Leu Ala Arg Gln
1 5 10 15

20 Glu Pro Ser Pro Ser Leu Gln Gly Cys Ser Glu Ser Pro Val Gly Met
25 30

25 Asp

30 (2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu
1 5 10 15

40 Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser
20 25

45 (2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Pro Gly Lys Pro Gln Ala Cys Pro Glu Leu Thr Ser Val Leu Pro
1 5 10 15

55

(2) INFORMATION FOR SEQ ID NO: 503:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

5

Asn Lys Ser Leu Xaa Ser Cys Leu Phe Val Leu His Phe Val Leu His
1 5 10 15

10

Cys Xaa Phe

15

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Lys Thr His Arg Leu Arg Ile Arg Asn Pro Cys Leu Gln Phe
1 5 10 15

25

Ser Ile Leu Asn Leu Phe Leu Leu Lys Met Ile Val Ser
20 25

30

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln
1 5 10 15

40

Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu
20 25 30

45

Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly
35 40 45

Pro Ser Ser Phe Gln Asn Pro Ala Ser Ser Pro Ser Ser Trp Thr His
50 55 60

50

Glu Glu Glu Pro Gly Tyr Phe Pro Gln Tyr Xaa
65 70 75

55

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Leu Pro Leu Ala Glu Leu Lys Asn Trp Val
1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 507:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

15

Met Leu Trp Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu
1 5 10 15

20

Ser Asp Thr Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr
20 25 30

Gly Asp Val Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys
35 40 45

25

Thr Gly Val Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val
50 55 60

Ala Arg Lys Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe
65 70 75 80

30

Met Met Asp Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg
85 90 95

35

Val Leu Gln Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu
100 105 110

Ser His Ala Ala Arg Arg His Gln Arg Xaa Leu Leu Ala Ala Ile Asn
115 120 125

40

Ala Phe Arg Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val
130 135 140

Asn Ser Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu
145 150 155 160

45

Gln Gln Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp
165 170 175

50

Thr Leu Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala
180 185 190

Leu Gly Pro Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa
195 200 205

55

(2) INFORMATION FOR SEQ ID NO: 508:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

5 Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val
 1 5 10 15
 Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Pro Ala
 20 25 30
 10 Val Xaa Lys Lys
 35

15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

20 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

25 Met Ala Leu Val Ala Leu Phe Thr Gln Leu Met Arg Xaa Leu Gly Arg
 1 5 10 15
 Cys Pro Gln

30

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

40 Met Thr Phe Pro Phe Glu Lys Glu Asn Ser Cys Phe Gln Cys Leu Leu
 1 5 10 15
 Phe Asp Ser Trp Arg Glu Gln Thr Arg Thr Asn Ile Gln Pro Gln Arg
 20 25 30
 45

50

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

60 Met His Leu Leu Asp Phe Phe Arg Asp Leu Val Leu Leu Val Leu Leu
 1 5 10 15

Ala Leu Leu Asp Ser Phe Trp Leu Glu Val Gln Lys
20 25

5

(2) INFORMATION FOR SEQ ID NO: 512:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

15 Met Cys Leu Ile His Phe Ile Lys Ile Ile Leu Val Phe Ile Leu Lys
1 5 10 15

Leu Trp Leu Tyr Ser Gln Lys Cys Pro Lys
20 25

20

(2) INFORMATION FOR SEQ ID NO: 513:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

30

Met Ile His Val His Glu Trp Asn Asp Gln Met Leu Met Val Tyr Ile
1 5 10 15

35 Phe Leu Tyr Pro Val Ser Ile Thr Phe Leu Asn Leu Cys Ser Leu Thr
20 25 30

Cys

40

(2) INFORMATION FOR SEQ ID NO: 514:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

45

50 Leu Asn Glu Ser Tyr Val Ser Arg Ala Gly Gly Trp Phe Ser Met Phe
1 5 10 15

Xaa Leu Ile Phe Phe Leu Leu Ala Leu Gly Ser Xaa Leu Cys Leu Leu
20 25 30

55

Leu Cys Leu Pro Ser Phe Asn Lys Thr Arg Arg Lys Gln Lys Pro
35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

5
10 Ser Ser Lys Thr Pro Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly Ser
1 5 10 15
Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu Gly
20 25 30
15 Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp
35 40

20 (2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

30 Leu Asn Trp
1

(2) INFORMATION FOR SEQ ID NO: 517:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

40 Phe Ala Phe Cys Ala Glu Leu Met Ile Gln Asn Trp Thr Leu Gly Ala
1 5 10 15
45 Val Asp Ser Gln Met Asp Asp Met Asp Met Asp Leu Asp Lys Glu Phe
20 25 30
Leu Gln Asp Leu Lys Glu Leu Lys Val Leu Val Ala Asp Lys Asp Leu
35 40 45
50 Leu Asp Leu His Lys Ser Leu Val Cys Thr Ala Leu Arg Gly Lys Leu
50 55 60
Gly Val Phe Ser Glu Met Glu Ala Asn Phe Lys Asn Leu Ser Arg Gly
65 70 75 80
55 Leu Val Asn Val Ala Ala Lys Leu Thr His Asn Lys Asp Val Arg Asp
85 90 95
60 Leu Phe Val Asp Leu Val Glu Lys Phe Val Glu Pro Cys Arg Ser Asp
100 105 110

664

His Trp Pro Leu Ser Asp Val Arg Phe Phe Leu Asn Gln Tyr Ser Ala
 115 120 125
 5 Ser Val His Ser Leu Asp Gly Phe Arg His Gln Ala Ser Gly Thr Ala
 130 135 140
 Thr Trp Ala Pro Ser Ala Ala Ala Ser Cys Ala Cys Ile Met Thr Glu
 145 150 155 160
 10 Val Pro Pro Asn Ala Pro Pro Thr Leu Thr Ile Lys Leu Leu
 165 170

15

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

25 Met Trp Lys Asn Leu Gly Ser Gly Ser Val Phe Val Thr Trp Phe Ser
 1 5 10 15
 Leu Val Met Ile Leu Ser Gly Ile Gly Pro Leu Gly Asp Ala Glu Asp
 20 25 30
 30 Ser Ile Ser Asp Val Ser His Arg Leu Arg Pro
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

45 Phe Gln Phe Pro Leu Leu Thr Ile Ala Leu Gln Phe Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 520:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

55

Met His Tyr Val Ile Val Leu Ser Leu Phe Val Val Leu Glu Lys Lys
 1 5 10 15
 60 Asn Lys Met Gly Ser Asp Gly Cys Leu Arg Lys Asn Gly Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 521:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Arg Ser Ile Val Leu Arg Gly Ser Leu Phe Leu Phe Phe Ser
1 5 10 15

15

His Tyr Thr Leu Lys Leu Leu Ser Val Ile Lys Gln Thr Asn Arg Lys
20 25 30

Ile Val Trp Glu Lys Pro Cys Ile Arg Leu Phe Tyr Xaa Val Leu
35 40 45

20

(2) INFORMATION FOR SEQ ID NO: 522:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Leu Pro Val Leu Leu Cys Leu Thr Leu Pro Met Pro Leu Pro
1 5 10 15

35

Ser Ala Thr Ala Arg Gly Gly Asn Arg Thr
20 25

(2) INFORMATION FOR SEQ ID NO: 523:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Ser Ser Ile Pro Val Ser Ile Leu Ile Gly Met Lys Leu Ile Leu Tyr
1 5 10 15

50

Leu Leu Ile Thr Glu Ser Gly Ser His Glu Lys Lys Ser Phe Tyr Pro
20 25 30

Ser Phe Lys Tyr Met Phe Lys Ile Ile Ile Tyr Val Ser Ala Tyr Cys
35 40 45

55

Arg Thr Ala Leu Arg Ala Thr Val Ser His
50 55

60

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Asn Arg Thr Leu Leu Phe Leu Ile Leu Phe Val Leu Phe Gly Leu Gly
 1 5 10 15
 Tyr Gly Phe

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Phe Leu Leu Val Leu Ser Val Phe Cys Asp Phe Met Cys Ser Ile
 1 5 10 15
 Ala Pro Arg Cys His Ala Leu Ser Leu Val Ser Leu Arg Ala Gln His
 20 25 30
 Leu Ser Leu Phe Ile Thr Cys His
 35 40

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Leu Leu Phe Ile Leu Leu Thr Leu Ser Ser Gly Cys Arg Leu Leu
 1 5 10 15
 Val Ser Ser Trp Lys Thr Phe Leu Pro His Phe Ser Leu Pro Gly Pro
 20 25 30
 Arg Glu His Pro Glu Gly Ser Arg Thr Trp Phe Phe Arg Tyr Trp Glu
 35 40 45
 Pro Gly Ala His Cys Leu His Cys Ala
 50 55

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

5

Ala Arg Leu Leu Leu Phe Leu Ser Ser Val His Pro Ser Ile Met Pro
 1 5 10 15

10

Ser Cys Asn Gln Leu
 20

15

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Ser Leu Thr Ser Ser Leu Thr Phe Leu Ser His Ile Leu Leu Leu
 1 5 10 15

25

Pro Gln Lys Leu Gln Phe Leu Ser Trp Met Glu Arg Gln Gln Arg Cys
 20 25 30

30

Thr Gly Val Ala Lys Tyr Ala
 35

35

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Val Leu Arg Leu Ile Gln Leu Ile Phe Leu Ile Phe Phe Ile His
 1 5 10 15

45

Ile Ile Ile Leu Leu Ile Pro Gly Ser Arg Pro Cys Gly Ser Trp Val
 20 25 30

50

Asn Asp Arg Xaa Leu Gly Leu Arg Asp Val Thr His Leu Ile Tyr Leu
 35 40 45

55

His Trp Val His Gly His Leu Pro Trp Cys His Pro Tyr Ile Gln Val
 50 55 60

Glu Phe Ser Ala Leu Ile Glu Ser Thr Ala Gln Leu Gly Leu Pro Phe
 65 70 75 80

60

Ser Trp Val Arg Val Ile His Pro Phe Leu Val Leu Pro Cys Leu Tyr
 85 90 95

Ser Pro Gly Leu Lys Asn Gly Ile Phe Leu Phe Leu Leu Arg Ala Met
 100 105 110

Pro Gly Gly Met Phe Pro Gly Asn Leu Glu Ala Phe Arg Val Pro Val
 115 120 125

5

10 (2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser
 1 5 10 15

20

Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe
 20 25 30

25

Trp Gly Phe Gly Xaa Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr
 35 40 45

Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser
 50 55 60

30

His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln
 65 70 75 80

Pro Asn

35

(2) INFORMATION FOR SEQ ID NO: 531:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

45

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala
 1 5 10 15

50

Tyr Trp Thr Met
 20

(2) INFORMATION FOR SEQ ID NO: 532:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln Leu Lys Ile
 1 5 10 15

5 Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu Lys Ile Ile
 20 25 30

Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser Trp Ala Ile
 35 40 45

10 Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn Lys Thr Ala
 50 55 60

15 Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr
 65 70 75

20 (2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser
 1 5 10 15

30 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Xaa Ser Tyr Leu Trp
 20 25 30

Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Xaa Trp Ala Cys
 35 40 45

35 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu
 50 55 60

40

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe
 1 5 10 15

Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg
 20 25 30

55 Ile Leu Phe Phe Ile Val Phe
 35

60 (2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Leu

1

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Asp Gln Phe Lys Ile Phe Tyr Phe Leu Lys Ala Phe Phe Ala Cys

1

5

10

15

Cys Asn Val Gln Asp Pro Ser Pro Phe Met Gly Glu Thr Gly Ser Tyr

20

25

30

Leu Asn Ile Gly

35

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Phe Asp Phe Leu Ser Tyr Phe Lys Asp Leu Leu Ser Cys

1

5

10

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Gly Phe Gly Phe Val Leu Asn Ile Phe Ser Phe Phe Leu Xaa Pro

1

5

10

15

Pro Leu

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

Leu Leu Leu Trp Thr Leu Leu Ala Xaa Tyr Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu
 1 5 10 15

Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg
 20 25 30

Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe
 35 40 45

Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys
 50 55 60

Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe
 65 70 75 80

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu
 85 90 95

Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Xaa
 100 105

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Phe Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met
 1 5 10 15

Leu Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr
 20 25 30

Leu Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser
 35 40 45

Pro Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe
50 55 60

5 Trp Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr
65 70 75 80

Leu Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val
85 90 95

10

Asp Gly Glu Glu Leu Gln Met Glu Pro Val
100 105

15

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

25 Met Asp Arg Phe Thr Val Ala Gly Val Leu Pro Asp Ile Glu Gln Phe
1 5 10 15

Phe Asn Ile Gly Asp Ser Ser Ser Gly Leu Ile Gln Thr Val Phe Ile
20 25 30

30 Ser Ser Tyr Met Val Leu Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg
35 40 45

Tyr Asn Arg Lys Tyr Leu Met Cys Gly Gly Ile Ala Phe Trp Ser Leu
50 55 60

35

Val Thr Leu Gly Ser Ser Phe Ile Pro Gly Glu His Phe Trp Leu Leu
65 70 75 80

40 Leu Leu Thr Arg Gly Leu Val Gly Val Gly Glu Ala Ser Tyr Ser Thr
85 90 95

Ile Ala Pro Thr Leu Ile Ala Asp Leu Phe Val Ala Asp Gln Arg Thr
100 105 110

45 Gly Cys Ser Ala Ser Ser Thr Leu Pro Phe Arg Trp Ala Val Val Trp
115 120 125

Ala Thr Leu Gln Ala Pro Lys Xaa
130 135

50

(2) INFORMATION FOR SEQ ID NO: 543:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

60

Met Ala Gly Asp Trp His Trp Ala Leu Arg Val Thr Pro Gly Leu Gly
 1 5 10 15
 Val Val Ala Val Leu Leu Leu Phe Leu Val Val Arg Glu Pro Pro Arg
 5 20 25 30
 Gly Ala Val Glu Arg His Ser Asp Leu Pro Pro Leu Asn Pro Thr Ser
 35 40 45
 Trp Trp Ala Asp Leu Arg Ala Leu Ala Arg Asn Pro Ser Phe Val Leu
 10 50 55 60
 Ser Ser Leu Gly Phe Thr Ala Val Ala Phe Val Thr Gly Ser Leu Ala
 65 70 75 80
 15 Leu Trp Ala Pro Ala Phe Leu Leu Arg Ser Arg Val Val Leu Gly Glu
 85 90 95
 Thr Pro Pro Cys Leu Pro Gly Asp Ser Cys Ser Ser Ser Asp Ser Leu
 20 100 105 110
 Ile Phe Gly Leu Ile Thr Cys Leu Thr Gly Val Leu Gly Val Gly Leu
 115 120 125
 25 Gly Val Glu Ile Ser Arg Arg Xaa Arg His Ser Asn Pro Arg Ala Asp
 130 135 140
 Pro Leu Val Cys Ala Thr Gly Leu Leu Gly Ser Ala Pro Phe Leu Phe
 145 150 155 160
 30 Leu Ser Leu Ala Cys Ala Arg Gly Ser Ile Val Ala Thr Tyr Ile Phe
 165 170 175
 Ile Phe Ile Gly Glu Thr Leu Leu Ser Met Asn Trp Ala Ile Val Ala
 35 180 185 190
 Asp Ile Leu Leu Tyr Val Val Ile Pro Thr Arg Arg Ser Thr Ala Glu
 195 200 205
 40 Ala Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala Gly Ser Pro
 210 215 220
 Tyr Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn Trp Pro Pro
 225 230 235 240
 45 Ser Phe Leu Ser Glu Phe Arg Ala Leu Gln Phe Ser Leu Met Leu Cys
 245 250 255
 Ala Phe Val Gly Ala Leu Gly Gly Ala Leu Ser Trp Ala Pro Xaa Ser
 50 260 265 270
 Ser Leu Arg Pro Thr Ala Gly Gly His Ser Cys Thr Cys Arg Ala Cys
 275 280 285
 55 Cys Thr Lys Gln Gly Pro Gln Thr Thr Gly Leu Trp Cys Pro Ser Gly
 290 295 300
 Ala Ala Pro Pro Ala Cys Pro Trp Pro Val Cys Ser Ser Glu Arg Leu
 305 310 315 320
 60

Pro Leu Thr Tyr Leu His Ile Cys His Ser Xaa Pro Trp Ala His Pro
 325 330 335

5 Thr Lys Gly Leu Gly Leu Thr Pro Trp Pro Gly Pro Ala Ser Arg Gly
 340 345 350

Thr Leu Gly Arg Val Pro Ala Pro Arg His Tyr Xaa Gly Ser Ser Gly
 355 360 365

10 Glu Glu Val Gly Val Gln Glu Gly Asp Pro Ser Pro Gln Gly Xaa Pro
 370 375 380

Gln Gly Leu Gly Ala Ile Cys Asn Gly Ile Lys Phe Val Ala Arg Pro
 385 390 395 400

15 Gln Val Pro Ala Leu Val Phe Leu Trp Val Ala Ser Asp Leu Ala Pro
 405 410 415

20 Arg Leu His Pro Arg Ala Pro Glu
 420

(2) INFORMATION FOR SEQ ID NO: 544:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Phe Arg Phe Val Ile Cys Leu Phe Leu Trp Leu Val Leu Cys Arg
 1 5 10 15

35

Asp Ser Thr Ser Ala Ser Arg Ile Ala Leu Tyr Tyr Arg Ile Val Phe
 20 25 30

Leu Ile His Gln Cys Ser Ser
 35

40

(2) INFORMATION FOR SEQ ID NO: 545:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Pro Trp Xaa Ala Gln Leu Leu Asp Arg Thr Ile Gly Pro Leu
 1 5 10 15

55

Tyr Leu Leu Phe Val Gln Phe Ser Pro Ala Phe Ser Arg Thr Ser Pro
 20 25 30

Trp Arg Ser Pro Lys Asn Phe Arg Arg Leu Tyr Pro Pro Cys Thr Thr
 35 40 45

60

Ser Gly Cys Ala Ala Arg Trp Leu Phe Ser

50

55

5 (2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Gly Leu Ser Val Leu Leu Pro Leu Cys Leu Leu Gly Pro Gly Arg
 1 5 10 15

Phe Thr Ser Gly Gln Lys Pro Leu Asp Thr Pro Gly Leu Gly Val Pro
 20 25 30

Phe

25 (2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu
 1 5 10 15

35 Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr
 20 25 30

Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu
 35 40 45

40 Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe
 50 55 60

45 Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr
 65 70 75 80

Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala
 85 90 95

50 Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr
 100 105 110

Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln
 115 120 125

55 Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala
 130 135 140

60 Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu
 145 150 155 160

676

Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly
 165 170 175
 5 Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu
 180 185 190
 Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val
 195 200 205
 10 Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu
 210 215 220
 Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val
 15 225 230 235 240
 Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys
 245 250 255
 20 Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser
 260 265 270
 Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn
 275 280 285
 25 Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp
 290 295 300
 Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe
 30 305 310 315 320
 Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp
 325 330 335
 35 Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu
 340 345 350
 Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln
 355 360 365
 40

(2) INFORMATION FOR SEQ ID NO: 548:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:
 50 Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
 1 5 10 15
 55 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
 20 25 30
 Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
 35 40 45
 60 Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro

Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser
1 5 10 15

His Cys Trp Gly Leu Pro Leu Ala Cys Gly Thr Phe Val Gln Gly His
20 25 30

Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala
35 40 45

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

```
Met Leu Leu Ser Leu Ala Ala Phe Ser Val Ile Ser Val Val Ser Tyr  
1          5          10          15
```

Leu Ile Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys
20 25 30

Ser Val Ile Gln Ala Val Gln Lys Ser Glu Glu Gly His Pro Phe Lys
35 40 45

Ala Tyr Leu Asp Val Asp Ile Thr Leu Ser Ser Glu Ala Phe His Asn
50 55 60

Tyr Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile
65 70 75 80

Ile Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala
85 90 95

Val Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile
100 105 110

Thr Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val
115 120 125

Tyr Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg
130 135 140

Asp Gln Thr Lys Ser Ile Val Glu Lys Ile Gln Ala Lys Leu Pro Gly
 145 150 155 160

5 Ile Ala Lys Lys Lys Ala Glu Xaa
 165

10 (2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Ser Val Pro Phe His Leu Leu Val Val Leu Arg Ser Arg Ala Val Arg
 1 5 10 15

20 Ala Arg Arg Arg Arg Glu Pro Arg Ser Leu Pro Arg Pro Gly Asp Glu
 20 25 30

25 Glu Leu Gln Leu Leu Leu Cys Gly Ala Arg Ser Asp Phe Leu Glu Arg
 35 40 45

Cys Glu Glu Asp Trp Val Cys Leu Trp His His Ala Asp His Ala Ala
 50 55 60

30 Phe Pro Gly Ser Phe Gln Cys His Gln Cys Gly Phe Leu Pro His Pro
 65 70 75 80

Gly Ser Ser Leu Cys His His Gln Leu Gln Asp Leu Gln Val Arg His
 85 90 95

35 Pro Ser Cys Thr Glu Val Arg Arg Arg Pro Ser Ile Gln Ser Leu Pro
 100 105 110

40 Gly Arg Arg His Tyr Ser Val Leu Arg Ser Phe Pro
 115 120

(2) INFORMATION FOR SEQ ID NO: 552:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Val His Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp
 1 5 10 15

55 Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His
 20 25 30

Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile
 35 40 45

60

679

Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His
 50 55 60

Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu
 5 65 70 75 80

Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro
 85 90 95

Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg
 10 100 105 110

Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr
 115 120 125

Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn
 130 135 140

Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val
 145 150 155 160

Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser
 165 170 175

25 Leu

30 (2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu
 1 5 10 15

40 Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His
 20 25 30

Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys
 35 40 45

Thr Glu Gly Ile Pro Cys Ala Lys Ile Pro Glu Trp Val Thr His Leu
 50 55 60

50 Thr Trp Gln Thr Leu Lys Asn Ser
 65 70

55 (2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

5 Val Leu Arg Ile Ile Cys Leu Trp Pro Cys Gly Thr Thr Leu Pro Leu
 1 5 10 15
 Val Glu Lys Ala His Asp Ser His Ser Ala Asp Pro Val Cys Pro Gly
 20 25 30
 10 Leu Thr Ala His Leu Pro Val Leu Leu Tyr Val Gln Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 555:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Lys His Ala Asp Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser
 1 5 10 15
 25 Pro Leu Leu Met Thr Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu
 20 25 30
 Ser Leu Gly Pro Arg Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg
 35 40 45
 30 Gly Phe Met Ile Val Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr
 50 55 60
 Ile Val Tyr Glu Phe Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp
 65 70 75 80
 Arg Cys Asp Pro Gln Asp Cys Thr Leu Gly Gln Cys Pro Ser Val Pro
 85 90 95
 40 Ser Pro Xaa Thr Pro Val Thr Lys Ala Tyr Val Val Arg Thr Glu Gln
 100 105 110
 Gly Thr Gly Pro Pro Leu Pro Thr Ala Ala Leu Gln Gly Pro Arg Leu
 115 120 125
 45 Trp Phe Leu Thr His Phe Pro Arg Ala Ala Pro Gly Met Trp Pro His
 130 135 140
 Cys Cys Leu Pro Leu Gln Ser Trp Gly Leu Lys Gly Leu Tyr Ser Tyr
 145 150 155 160
 Phe Pro Leu Pro Ala Leu Lys Leu Gly Arg Gly Ala Leu Arg Ala Gly
 165 170 175
 55 Pro Thr Lys Gly Leu Val Ala Phe Phe Leu Thr Gln Lys Arg Ser Ala
 180 185 190
 Ile Met Ser Leu Trp Thr Gln Ser His Ser Ser Thr Pro His Thr Glu
 195 200 205
 60

Ala Val Ala Ser Gly Pro Lys Val Arg Val Gly Gly Gly Leu Gly Ile
 210 215 220

5 Gln Pro Val Glu Ala Ala Tyr Ser Thr Cys Val Leu Ile Lys Ser Asp
 225 230 235 240

Arg Gly Asn His Glu Lys Lys Lys Lys Lys
 245 250

10

(2) INFORMATION FOR SEQ ID NO: 556:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

20 Gly Leu Ala Gly Leu Cys Gly Gln Leu Ser Ser Pro Ala Leu Cys Val
 1 5 10 15

Asn Arg Leu

25

(2) INFORMATION FOR SEQ ID NO: 557:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

35 Met Ile Thr Glu Lys Trp Gly Leu Asn Met Glu Tyr Cys Arg Gly Gln
 1 5 10 15

40 Ala Tyr Ile Xaa Ser Ser Gly Phe Ser Ser Lys Met Lys Val Val Ala
 20 25 30

Ser Arg Leu Leu Glu Lys Tyr Pro Gln Ala Ile Tyr Thr Leu Cys Ser
 35 40 45

45 Ser Cys Ala Leu Asn Met Trp Leu Ala Lys Ser Val Pro Val Met Gly
 50 55 60

50 Val Ser Val Ala Leu Gly Thr Ile Glu Glu Val Cys Ser Phe Phe His
 65 70 75 80

Arg Ser Pro Gln Leu Leu Leu Glu Leu Asp Asn Val Ile Ser Val Leu
 85 90 95

55 Phe Gln Asn Ser Lys Glu Arg Gly Lys Glu Leu Lys Glu Ile Cys His
 100 105 110

Ser Gln Trp Thr Gly Arg His Asp Ala Phe Glu Ile Leu Val Glu Leu
 115 120 125

60 Leu Gln Ala Leu Val Leu Cys Leu Asp Gly Ile Asn Ser Asp Thr Asn

130 135 140

Ile Arg Trp Asn Asn Tyr Ile Ala Gly Arg Ala Phe Val Leu Cys Ser
 145 150 155 160

5 Ala Val Ser Asp Phe Asp Phe Ile Val Thr Ile Val Val Leu Lys Asn
 165 170 175

10 Val Leu Ser Phe Thr Arg Ala Phe Gly Lys Asn Leu Gln Gly Gln Thr
 180 185 190

Ser Asp Val Phe Phe Ala Ala Gly Ser Leu Thr Ala Val Leu His Ser
 195 200 205

15 Leu Asn Glu Val Ile Gly Lys Tyr Xaa
 210 215

20 (2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu Asn Glu
 1 5 10 15

30 Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg Asn Thr
 20 25 30

35 Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile Asn Phe
 35 40 45

Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile Lys Leu
 50 55 60

40 Tyr Thr Ser Lys Ser Glu Leu Pro Thr Asp Asn Ser Glu Thr Val Glu
 65 70 75 80

Asn Thr

45

(2) INFORMATION FOR SEQ ID NO: 559:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Val Leu Ile Leu Leu Asn Leu Leu Leu Gly Gln Phe Ser Cys Met
 1 5 10 15

60 Ser Pro Ala Ser His His Cys His Pro Leu Pro Thr Glu Met Pro Cys
 20 25 30

Ser Ser Asp Trp Gly Phe Asp Ser His Thr Val Tyr Pro Ser Cys Val
 35 40 45

5 Asp Ala Leu Leu Pro Lys Pro Ser Ala Asn Ser Phe Pro Asn Gly Ser
 50 55 60

Cys His Cys Gln Gly Leu Tyr Asn Gln Gln Gln Asn Leu His Ala
 65 70 75 80

10 Ala Glu Gly Pro Ala Ser Leu Arg Cys Asn Lys Tyr Val Ser Thr
 85 90 95

15

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

20 Met Ile Pro Ala Tyr Ser Lys Asn Arg Ala Tyr Ala Ile Phe Phe Ile
 1 5 10 15

Val Phe Thr Val Ile Gly Asp Ala Pro Gly Ala Val Leu Ser Cys Ala
 20 25 30

30 Gly His Pro Cys Val Gly Phe Ala Ala Val Leu Val Ala Pro Leu Thr
 35 40 45

Val Ala Val Ser Ser Xaa
 50

35

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

40

45 Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 1 5 10 15

50 Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
 20 25 30

Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro
 35 40 45

55 Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys
 50 55 60

Asp Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu
 65 70 75 80

60

Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg Ile
85 90 95

5 Asn Val Gly Leu Arg Gly Trp Trp Leu Val Ala Xaa
100 105

10 (2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys
1 5 10 15

20 Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala
20 25 30

Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg
35 40 45

25 Ala Pro
50

30 (2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
1 5 10 15

Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
20 25 30

45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
35 40 45

Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
50 55 60

Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
65 70 75 80

55 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
85 90 95

Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
100 105 110

60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

685

115 120 125

Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg
130 135 140

5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Leu Glu Asp Arg
145 150 155 160

10 Lys Tyr Glu Tyr Leu Met Thr Leu His Gly Val Val Asn Glu Ser Thr
165 170 175

Val Cys Leu Met Gly His Glu Arg Arg Gln Thr Leu Asn Leu Ile Thr
180 185 190

15 Met Leu Ala Ile Arg Val Leu Ala Asp Gln Asn Val Ile Pro Asn Val
195 200 205

Ala Asn Val Thr Cys Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala
210 215 220

20 Asn Phe Ser Asn Tyr Tyr Ile Ala Gln Val Gln Pro Val Phe Thr Cys
225 230 235 240

25 Gln Gln Gln Thr Tyr Ser Thr Trp Leu Pro Cys Asn Xaa
245 250

30 (2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Ser Phe Leu Met Trp Leu Met Ser Leu Ala Ile Thr Ser Gln Pro
1 5 10 15

40 Pro Met

45 (2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
1 5 10 15

55 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
20 25 30

60 Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
35 40 45

Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
 50 55 60

5 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Phe
 65 70 75 80

10

(2) INFORMATION FOR SEQ ID NO: 566:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

20

His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln Val Leu Ser
 1 5 10 15

25

Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu Ala Pro Gly Arg
 20 25 30

Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro Trp Phe Thr Ala
 35 40 45

30

Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys Arg Gln Arg Arg
 50 55 60

Gln Glu Arg Arg Gln Met Lys Arg Leu
 65 70

35

(2) INFORMATION FOR SEQ ID NO: 567:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

45

Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys Lys Glu Glu Val Ile
 1 5 10 15

50

Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp Val Tyr Tyr Phe Ser
 20 25 30

Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln Leu Ala Arg Tyr Leu
 35 40 45

55

Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe Arg Thr Gly Lys Met
 50 55 60

Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn Asp Pro
 65 70 75 80

60

Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu Pro Ile
 85 90 95
 5 Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val Thr Asn
 100 105 110
 His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn Glu Gln
 115 120 125
 10 Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser Ala Ser
 130 135 140
 Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys Gly Leu
 15 145 150 155 160
 Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser Ala Val
 165 170 175
 20 Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln Val Ser
 180 185 190
 Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser Gln Pro
 195 200 205
 25 Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys Gln Glu
 210 215 220
 Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu Met Ala
 30 225 230 235 240
 Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile Glu Met
 245 250 255
 35 Asp Ser Gly Asp Glu Ala Xaa
 260

(2) INFORMATION FOR SEQ ID NO: 568:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Met Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala
 1 5 10 15
 50 Leu Arg Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Leu
 20 25 30
 Leu Phe Gly Leu Thr His Leu Asn Pro Ser Ala Lys Leu Leu Leu Ser
 35 40 45
 55 Gln Met Lys Thr Ser Gly Asn Arg Lys Ser Glu Tyr Ser Lys Tyr Ala
 50 55 60
 60 Arg Asn Trp Lys Lys His
 65 70

(2) INFORMATION FOR SEQ ID NO: 569:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Pro Val Thr Ser Lys Arg Thr Leu Phe Phe Pro Asp Pro Cys Ser
1 5 10 15

15

Tyr Asp Thr Pro Pro Pro Asp Cys His Cys His Ser Phe Arg Ala Glu
20 25 30

Leu Leu

20

(2) INFORMATION FOR SEQ ID NO: 570:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
1 5 10 15

35

Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
20 25 30

Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
35 40 45

40

His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ser
50 55 60

45

Lys Ala Pro Asn Ser Leu Gly Thr Thr Gly Leu Trp Ser Thr Val Tyr
65 70 75 80

Ile Phe Thr Glu Val Phe His Asn Phe Ser Asn Asn Ser Ile Phe Ser
85 90 95

50

Gly Lys Phe Leu Tyr Glu Val Xaa
100

(2) INFORMATION FOR SEQ ID NO: 571:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu Leu His Ile Val Leu
1 5 10 15

5 Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala Trp Thr Leu Thr Asn
20 25 30

Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu His Ala Val Lys Gly
35 40 45

10

Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His
50 55 60

15

Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr Ser Ser Arg Lys Phe
65 70 75 80

Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu Ala Ser Phe Tyr Thr
85 90 95

20

Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr Ala Ser Leu Leu Ser
100 105 110

Val Leu Ile Pro Lys Met Pro Gln Leu His Gly Val Arg Ile Phe Gly
115 120 125

25

Ile Asn Lys Tyr
130

30

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

40 Met Asn Lys Trp Ile Cys Glu Met His Cys Tyr Leu Val Leu Leu Ser
1 5 10 15

Val Cys Ser Pro Ser Ala Leu Arg Arg Val Arg His Thr Leu Ser Arg
20 25 30

45

50

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Pro Val Leu Ser Leu Leu Cys Thr Leu Ile Val Ser Phe Gln Ser
1 5 10 15

60

Ala Asp Ser Cys Glu Val Phe Leu Asn Cys Ser Leu
20 25

5

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

15

Met Lys Val Ser Thr Met Leu Trp Phe Leu Cys Trp Glu Gln Ser His
1 5 10 15

Phe Leu Arg Glu Trp Glu Asp Leu Ser Thr Phe Leu Ile Leu Ile Gln
20 25 30

20

Met Glu Cys Gln Tyr Gly Asn Ser
35 40

25

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

30

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

35

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser
1 5 10 15

Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Xaa Leu
20 25 30

40

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

45

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

50

Met Lys Arg Gly Cys Leu Gly Leu Leu Phe Phe Ser Cys Cys Ser Ser
1 5 10 15

Ala Pro Thr Met Leu Leu Cys Asp Tyr Leu Asn Trp Phe
20 25

55

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

5 Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser Val
 1 5 10 15

Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu Leu
 20 25 30

10 Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu Lys
 35 40 45

Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val Lys
 15 50 55 60

Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Xaa Asn Arg Arg Arg
 65 70 75 80

20 Xaa Val Arg Gly Leu Pro Ser Xaa Leu Thr Asn Ser
 85 90

25 (2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg
 1 5 10 15

35 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg
 20 25 30

Arg Val Met Val Asn Leu Asn Ile Leu Phe
 40 35 40

45 (2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val
 1 5 10 15

55 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Pro Pro Leu Ser
 20 25 30

Thr Phe Thr Ser Asp Phe Tyr Phe Met Glu Phe Gly Ile Glu Val Lys
 35 40 45

60

Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr Lys
 50 55 60

5 Lys Phe Asn Lys Lys Lys
 65 70

10 (2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

Met Leu Arg Leu Leu Leu Val Ala Phe Ala Leu Val Val Val Leu
 1 5 10 15

20 Phe His Val Leu Leu Ala Pro Ile Thr Ala Leu Phe His Thr His Phe
 20 25 30

Tyr Asp Arg Leu Gln Asp Ala Gly Ser Arg Trp Pro Glu Leu Tyr Leu
 35 40 45

25 Tyr Ser Arg Ala Asp Glu Val Val Leu Ala Arg Asp Ile Glu Arg Met
 50 55 60

30 Val Glu Ala Arg Leu Ala Arg Arg Val Leu Ala Arg Ser Val Asp Phe
 65 70 75 80

Val Ser Ser Ala His Val Ser His Leu Arg Asp Tyr Pro Thr Tyr Tyr
 85 90 95

35 Thr Ser Leu Cys Val Asp Phe Met Arg Asn Cys Val Arg Cys
 100 105 110

40 (2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

Met Phe Lys Leu Glu Glu Cys Gly Lys Thr Thr Phe Leu Leu Ser Met
 1 5 10 15

50 Ala Leu Tyr Phe Trp Trp Ile Val Gln Thr Thr Lys Gly Cys
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

60 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

5 Met Glu Ser Asp Ala Leu Leu Leu Thr Ile Phe Trp Ile Ile Ala Arg
 1 5 10 15
 Ser Ser Val Arg Ser Val Gly Lys Ser Ser Gln Arg Ser Phe Thr Thr
 20 25 30
 10 Ile Thr Gln Leu Arg Ser Thr His Thr Gly Pro Ser Arg Arg Ser Tyr
 35 40 45
 Leu Ile Trp Trp Asn Gly Gly Pro Lys Arg Thr Ile Ser Tyr Val Ser
 50 55 60
 15 Arg Arg Phe Arg Ser Phe Arg
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

25

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

30 Val Gly Leu Phe Gln Pro Lys Thr Phe Gln Val Pro Val Thr Asp Leu
 1 5 10 15
 Tyr Ile Phe Ile Lys Ile Tyr Ser Glu Ile Gly Pro Ile Met His Val
 20 25 30
 35 Leu Cys Pro Gly Tyr Ser Gln Ser Pro Ser Thr Pro Pro Trp Thr
 35 40 45

40

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

50 Met Trp Phe Gly Ser Asp Arg Ser Asp Leu Arg Ile Gly Thr Ala Phe
 1 5 10 15
 Leu Phe Asp Leu Val Cys Asp Leu Cys Ile His Ala Trp Lys Pro Pro
 20 25 30
 55 Gly Leu Val Arg Phe Ser Phe
 35

60

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Leu Asn Thr Ala Ser Leu Asn Leu Pro Trp Lys Val Gln Leu Phe
1 5 10 15

10 Ala His Ala

15 (2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Ala Cys Leu Leu Phe Leu Ala Phe Ser Trp Lys Arg Lys
1 5 10 15

25 Gly Leu Trp Ser Gly Pro Gly
20

30 (2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

40 Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser
1 5 10 15

Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val
20 25 30

45 Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro
35 40 45

Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln
50 55 60

50 Ala His Thr Val Ala
65

55 (2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

60 (B) TYPE: amino acid

695

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

5 Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
 1 5 10 15

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
 20 25 30

10 Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu
 35 40 45

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
 50 55 60

15 Arg Lys Lys Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys
 65 70 75

20

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

30 Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
 1 5 10 15

Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
 20 25 30

35 Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
 35 40 45

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
 50 55 60

40 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro
 65 70 75 80

45 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
 85 90 95

Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
 100 105 110

50 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly
 115 120 125

Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
 130 135 140

55 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa
 145 150 155

60

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

Met Pro Glu Thr Arg Leu Gly His Arg Gln Gln Phe Ala Val Phe His
1 5 10 15

Leu Xaa Pro Val Pro Pro Cys Gly
20

15

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Leu Thr Phe Leu Phe Ser Ala Cys Ala Thr Cys Leu Gly Lys Leu
1 5 10 15

Ala Ser Pro Leu Ala Pro Val Gly Pro Gln Gln Arg Gly Xaa Pro Pro
20 25 30

30

Gly Pro Pro Leu Leu Ser
35

35

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

Met Asp Pro Phe His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu
1 5 10 15

Val Phe Ala Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser
20 25 30

Arg Arg Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp
35 40 45

Glu Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro
50 55 60

55

Gln Lys Ala Glu Asn
65

60

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

10 Asn Leu Arg Val Arg Leu Gly Asp Val Ile Ser Ile Gln Pro Cys Pro
 1 5 10 15

 Asp Val Lys Tyr Gly Lys Arg Ile His Val Leu Pro Ile Asp Asp Thr
 20 25 30

15 Val Glu Gly Ile Thr Gly Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr
 35 40 45

 Phe Leu Glu Ala Tyr Arg Pro Ile Arg Lys Gly Asp Ile Phe Leu Val
 50 55 60

20 Arg Gly Gly Met Arg Ala Val Glu Phe Lys Val Val Glu Thr Asp Pro
 65 70 75 80

 Ser Pro Tyr Cys Ile Val Ala Pro Asp Thr Val Ile His Cys Glu Gly
 85 90 95

 Glu Pro Ile Lys Arg Glu Asp Glu Glu Glu Ser Leu Asn Glu Val Gly
 100 105 110

30 Tyr Asp Asp Ile Gly Gly Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu
 115 120 125

 Met Val Glu Leu Pro Leu Arg His Pro Ala Leu Phe Lys Ala Ile Gly
 130 135 140

35 Val Lys Pro Pro Arg Gly Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly
 145 150 155 160

 Lys Thr Leu Ile Ala Arg Ala Val Ala Asn Glu Thr Gly Ala Phe Phe
 165 170 175

 Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys Leu Ala Gly Glu Ser
 180 185 190

45 Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro
 195 200 205

 Ala Ile Ile Phe Ile Asp Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu
 210 215 220

50 Lys Thr His Gly Glu Val Glu Arg Arg Ile Val Ser Gln Leu Leu Thr
 225 230 235 240

 Leu Met Asp Gly Leu Lys Gln Arg Ala His Val Ile Val Met Ala Ala
 245 250 255

 Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg
 260 265 270

60 Phe Asp Arg Glu Val Asp Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu

275 280 285
 Glu Ile Leu Gln Ile His Thr Lys Asn Met Lys Leu Ala Asp Asp Val
 290 295 300
 5 Asp Leu Glu Gln
 305

10

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 15 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

20 Met Gln Ile Lys Leu Leu Lys Ser Val Lys Thr Val Phe Ala Ile Thr
 1 5 10 15
 Leu Leu Val Leu Phe Leu
 20

25

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

35 Met Phe Pro Lys Phe Cys Pro Ile Leu Ser Leu Val Asp Phe Ile Ser
 1 5 10 15
 His Arg Asp Lys Pro Glu Thr Glu
 20

40

(2) INFORMATION FOR SEQ ID NO: 596:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

50

Met Leu Ile Glu Cys Ala Trp Gln Leu Met Phe Leu Leu Leu Lys Val
 1 5 10 15
 55 Glu Gln Leu Gly Ile Leu Asp Lys
 20

60

(2) INFORMATION FOR SEQ ID NO: 597:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:
- Met
 1
- 10
- (2) INFORMATION FOR SEQ ID NO: 598:
- (i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:
- 20 Met Cys Ile Met Ser Ala Leu Val
 1 5
- 25 (2) INFORMATION FOR SEQ ID NO: 599:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
30 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:
- Met Phe Leu Val Trp Phe Phe Trp Gly Leu Ile Ser Ala Leu Ser Asn
 1 5 10 15
- 35 Val His Thr Pro Ser Arg Leu Pro Ala
 20 25
- 40
- (2) INFORMATION FOR SEQ ID NO: 600:
- (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:
- Met Xaa Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser
50 1 5 10 15
- Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly
 20 25
- 55
- (2) INFORMATION FOR SEQ ID NO: 601:
- (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 61 amino acids

700

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

5 Met Trp Thr Arg Ser Ser Arg Cys Leu Leu Cys Ile Pro Gly Xaa
 1 5 10 15

Ser Arg Arg Arg Arg Ala Gly Ser Gly Met Lys Pro Arg Ser Trp Ser
 20 25 30

10 Ala Trp Arg Pro Ser Gly Gly Thr Gly Thr Ser Ser Ser Gln Ser Ser
 35 40 45

15 Thr Gln Ser Arg Thr Leu Ser Ala Thr Ala Ser Pro Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 602:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu
 1 5 10 15

30 Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr
 20 25

35 (2) INFORMATION FOR SEQ ID NO: 603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

Met Pro Pro Lys Gln Glu Leu Gly Ser Gly Val Gly Glu Leu Ala Lys
 1 5 10 15

45 Asn Ser Lys Arg Gln His Trp Asn His Arg Trp Lys Lys Tyr Leu Lys
 20 25 30

50 Leu Ile Arg Trp Glu Asp Gly Leu Leu Leu Glu Gly Leu Leu Leu Val
 35 40 45

Leu Glu His Cys Ala Thr Met Ala Trp Asp Cys Leu Met Arg Leu Glu
 50 55 60

55 Leu Leu Lys Arg Leu
 65

60 (2) INFORMATION FOR SEQ ID NO: 604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

Lys Ile Val Tyr Ile Leu Gly Asn Pro Leu Lys Phe Asn Ser Arg Val
 1 5 10 15
 Ile His His Leu Val Leu Leu Gln
 20

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

Met Asn Leu His Gln Arg Arg Leu Leu Leu Ile Gly His Leu Met Thr
 1 5 10 15
 Leu Val Lys Ala Ser Lys Ser Phe Ser Phe Thr Glu Ile Thr Ser Ser
 20 25 30
 Arg Lys Lys
 35

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr
 1 5 10 15
 Tyr Asn Ile His Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val
 20 25 30
 Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr
 35 40 45
 Val Gly Pro Thr Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu
 50 55 60
 His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Xaa
 65 70 75 80
 Glu Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln
 85 90 95

Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro
 100 105 110

5 Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln
 115 120 125

Ser His
 130

10

(2) INFORMATION FOR SEQ ID NO: 607:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

20 Met Leu Val Ile Phe Leu Phe Thr Ser Leu Leu Lys Ile Pro Ser Ser
 1 5 10 15

Val Pro Gly Leu Ile Asn Val
 20

25

(2) INFORMATION FOR SEQ ID NO: 608:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

35

Glu Leu Asp Tyr Ile Leu
 1 5

40

(2) INFORMATION FOR SEQ ID NO: 609:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

50 Met Ala Pro Pro Gly Trp Gln Xaa Xaa Xaa Xaa Xaa Trp Leu Ala Cys
 1 5 10 15

Pro Asp Arg Gly Glu Leu Ser Ser Arg Ser Pro Pro Cys Arg Leu Ala
 20 25 30

55 Arg Trp Ala Glu Gly Asp Arg Glu Thr Arg Thr Cys Leu Leu Glu Leu
 35 40 45

Ser Ala Gln Ser Trp Gly Gly Arg Phe Arg Arg Ser Ser Ala Val Ser
 50 55 60

60

703

Ala Gly Ser Pro Ser Arg Leu His Phe Leu Pro Gln Pro Leu Leu Leu
65 70 75 80

Arg Ser Ser Gly Ile Pro Ala Ala Ala Thr Pro Trp Pro Gln Pro Ala
5 85 90 95

Gly Leu Pro Val Arg Pro Thr Pro Thr Arg Thr Gly Glu Glu Asp Arg
100 105 110

Thr Leu Asp Ile Ser Ile Cys Thr Glu Val Leu Ala Gly Thr Glu Gln
10 115 120 125

Pro Pro Pro Pro Arg Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg
130 135 140

Leu Glu Thr Leu Asp Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg
145 150 155 160

Gly Lys Leu Asp Phe Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe
20 165 170 175

Gln Gly Glu Asp Arg Lys Phe Ala Pro Ser Asp Lys Ser Gln Pro Pro
180 185 190

Thr Thr Glu Arg Glu Gln Val Pro Val Ser Arg Ile Gln Thr Asp Leu
25 195 200 205

Thr Glu Ile Gly Ser Ser Met Arg Ser Pro Gly Val Ser Pro Arg Ile
210 215 220

Trp Leu Asp Phe Gln Ser Thr Xaa
30 225 230

35

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids
40 (B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

Met Val Leu Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu
45 1 5 10 15

Leu Leu Asn Met Leu Ile Ala Leu Met Xaa Arg Asp Arg Gln Gln Cys
20 25 30

50 Arg His

55

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids
60 (B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

5 Met Val Phe Glu Gly Phe Ser Ser Ala Phe Cys Leu Ser Ser Thr Ala
 1 5 10 15
 Pro Thr Ser His Pro
 20

10

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

20 Gly Lys Lys Asn Gln Leu Leu Val Ile
 1 5

25

(2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val
 1 5 10 15

35

Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys
 20 25

40

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

45

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

Met Ala Lys Arg Ser Pro Gly Gly Cys Gly Ser Gly Leu Ile Leu Leu
 1 5 10 15

50

Cys Cys Gln Pro Cys Arg Pro Thr Ser Ser Ala Pro Met Arg
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

5 Ile Thr Ile Ala Ile Gln Met Ile Cys Leu Val Asn Xaa Glu Leu Tyr
 1 5 10 15
 Pro Thr Phe Val Arg Asn Xaa Gly Val Met Val Cys Ser Ser Leu Cys
 20 25 30
 10 Asp Ile Gly Gly Ile Ile Thr Pro Phe Ile Val Phe Arg Leu Arg Glu
 35 40 45
 Val Trp Gln Ala Leu Pro Leu Ile Leu Phe Ala Val Leu Gly Leu Leu
 50 55 60
 15 Ala Ala Gly Val Thr Leu Leu Leu Pro Glu Thr Lys Gly Val Ala Leu
 65 70 75 80
 Pro Glu Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys Pro
 20 85 90 95
 Lys Glu Asn Thr Ile Tyr Leu Lys Val Gln Thr Ser Glu Pro Ser Gly
 100 105 110
 25 Thr

30 (2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

35 Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys Pro Lys Glu
 1 5 10 15
 40 Asn Thr

45 (2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

50 Pro Arg Val Arg Asn Ser Pro Glu Asp Leu Gly Leu Ser Leu Thr Gly
 1 5 10 15
 Asp Ser Cys Lys Leu
 20
 60

(2) INFORMATION FOR SEQ ID NO: 618:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

10 Gln Ala Asp Asp Leu Gln Ala Thr Val Ala Ala Leu Cys Val Leu Arg
 1 5 10 15

Gly Gly Gly Pro Trp Ala Gly Ser Trp Leu Ser Pro Lys Thr Pro Gly
 20 25 30

15 Ala Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg
 35 40 45

Lys Arg Leu Leu
 20 50

(2) INFORMATION FOR SEQ ID NO: 619:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu Ala Xaa Xaa
 1 5 10 15

35 Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp Phe Gly Gly
 20 25 30

Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr Leu Trp Leu
 35 40 45

40 Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val Val Pro Gly
 50 55 60

45 Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val Met Gly Val
 65 70 75 80

Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys Leu Glu Phe
 85 90 95

50 Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Ile Gln Tyr
 100 105 110

Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln Glu Ala Trp
 115 120 125

55 Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala Ala Arg Xaa
 130 135 140

60 His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg Gln Val Arg
 145 150 155 160

[illegible]

20 (2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly
 1 5 10 15
 30 Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser
 20 25 30
 Gly Ala Gly Lys
 35

(2) INFORMATION FOR SEQ ID NO: 621:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

```

Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu
  1             5             10             15

Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser
50          20          25          30

Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala
          35          40          45

55 His Lys Ala Lys Ser His Pro Glu Val
    50          55

```

60 (2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln
1 5 10 15

Pro Ser Asp

(2) INFORMATION FOR SEQ ID NO: 623:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

Asn Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser
1 5 10 15

Lys Ser Tyr

(2) INFORMATION FOR SEQ ID NO: 624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys Ile Phe
1 5 10 15

Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met Asn Ser
20 25 30

Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser Asp Ser
35 40 45

Ala Gly Pro
50

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

Ile Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala
 1 5 10 15

5 His Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys
 20 25 30

Lys Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu
 35 40 45

10 Gln Lys Gln Leu Leu Arg His Ala Lys His His Thr
 50 55 60

15 (2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

25 Asp Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser
 1 5 10 15

Ser His Asn Leu Ala Val His Arg Met Ile His Thr Gly Glu Lys
 20 25 30

30 (2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

40 Arg Ser Ser Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile Cys Lys Ser
 1 5 10 15

Glu Pro Asn Thr Asp Gln Leu Asp Tyr
 20 25

45 (2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

55 Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu
 1 5 10 15

60 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser
 20 25 30

Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala
 35 40 45
 5 His Lys Ala Lys Ser His Pro Glu Val Xaa Ile Thr Ser Thr Asp Ile
 50 55 60
 Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln Pro Ser Asp Xaa Asn Ser
 65 70 75 80
 10 Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser Lys Ser
 85 90 95
 Tyr Xaa Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys
 15 100 105 110
 Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met
 115 120 125
 20 Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser
 130 135 140
 Asp Ser Ala Gly Pro Xaa Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala
 25 145 150 155 160
 Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met Ile His
 165 170 175
 30 Thr Gly Glu Lys His Tyr Xaa
 180

- 35 (2) INFORMATION FOR SEQ ID NO: 629:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His
 1 5 10 15
 45 Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys
 20 25 30
 Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln
 35 40 45
 50 Lys Gln Leu Leu Arg His Ala Lys His His Thr Asp
 50 55 60

- 55 (2) INFORMATION FOR SEQ ID NO: 630:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 60 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

5 Pro Phe Lys Asp Asp Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu
 1 5 10 15

Arg Glu Thr Pro Lys Pro Arg Arg Lys Ser Gly
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

20 Glu Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu
 1 5 10 15

Met Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val
 20 25 30

25 Leu Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu
 35 40 45

30 Trp Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg
 50 55 60

Met Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val
 65 70 75 80

35 Gln Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu
 85 90 95

Asn Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met
 100 105 110

40

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

50

Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg Pro Thr Gly Gln Gln
 1 5 10 15

55 Leu Glu Ser Leu Gly Leu Leu Ala
 20

60

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

Val His Arg Glu Glu Ala Ser Cys Tyr Cys Gln Ala Glu Pro Ser Gly
 1 5 10 15

10 Asp Leu

15 (2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

Arg Pro Ala Leu Arg Gln Ala Gly Gly Gly Thr Arg Glu Pro Arg Gln
 1 5 10 15

25 Lys Arg Trp Ala Gly Leu
 20

30

(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

Ala Val Asn Phe Arg Pro Gln Arg Ser Gln Ser Met
 1 5 10

40

(2) INFORMATION FOR SEQ ID NO: 636:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met Leu Gly Val
 1 5 10 15

55 Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val Ala Val Asn Asn
 20 25 30

Pro Lys Lys Gln Glu
 35

60

(2) INFORMATION FOR SEQ ID NO: 637:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

Glu Glu Met Ala Asp Ser Val Lys Thr Phe Leu Gln Asp Leu Ala Arg
 1 5 10 15

15

Gly Ile Lys Asp Ser Ile Trp Gly Ile Cys Thr Ile Ser Lys Leu Asp
 20 25 30

Ala Arg Ile Gln Gln Lys Arg Glu Glu Gln Arg Arg Arg Ala Ser
 35 40 45

20

Ser Val Leu Ala Gln Arg Arg Ala Gln Ser Ile Glu Arg Lys Gln Glu
 50 55 60

25

Ser Glu Pro Arg Ile Val Ser Arg Ile Phe Gln Cys Cys Ala Trp Asn
 65 70 75 80

Gly Gly Val Phe Trp Phe Ser Leu Leu Leu Phe Tyr Arg Val Phe Ile
 85 90 95

30

Pro Val Leu Gln Ser Val Thr Ala Arg Ile Ile Gly Asp Pro Ser Leu
 100 105 110

His Gly Asp Val Trp Ser Trp Leu Glu Phe Phe Leu Thr Ser Ile Phe
 115 120 125

35

Ser Ala Leu Trp Val Leu Pro Leu Phe Val Leu Ser Lys Val Val Asn
 130 135 140

40

Ala Ile Trp Phe Gln Asp Ile Ala Asp Leu Ala Phe Glu Val Ser Gly
 145 150 155 160

Arg Lys Pro His Pro Phe Pro Ser Val Ser Lys Ile Ile Ala Asp Met
 165 170 175

45

Leu Phe Asn Leu Leu Leu Gln Ala Leu Phe Leu Ile Gln Gly Met Phe
 180 185 190

Val Ser Leu Phe Pro Ile His Leu Val Gly Gln Leu Val Ser Leu Leu
 195 200 205

50

His Met Ser Leu Leu Tyr Ser Leu Tyr Cys Phe Glu Tyr Arg Trp Phe
 210 215 220

55

Asn Lys Gly Ile Glu Met His Gln Arg Leu Ser Asn Ile Glu Arg Asn
 225 230 235 240

Trp Pro Tyr Tyr Phe Gly Phe Gly Leu Pro Leu Ala Phe Leu Thr Ala
 245 250 255

60

Met Gln Ser Ser Tyr Ile Ile Ser Gly Cys Leu Phe Ser Ile Leu Phe
 260 265 270

Pro Leu Phe Ile Ile Ser Ala Asn Glu Ala Lys Thr Pro Gly Lys Ala
 275 280 285

5 Tyr Leu Phe Gln Leu Arg Leu Phe Ser Leu Val Val Phe Leu Ser Asn
 290 295 300

Arg Leu Phe His Lys Thr Val Tyr Leu Gln Ser Ala Leu Ser Ser Ser
 305 310 315 320

10 Thr Ser Ala Glu Lys Phe Pro Ser Pro His Pro Ser Pro Ala Lys Leu
 325 330 335

Lys Ala Thr Ala Gly His
 15 340

(2) INFORMATION FOR SEQ ID NO: 638:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 529 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

Met Ala Lys Phe Met Thr Pro Val Ile Gln Asp Asn Pro Ser Gly Trp
 1 5 10 15

30 Gly Pro Cys Ala Val Pro Glu Gln Phe Arg Asp Met Pro Tyr Gln Pro
 20 25 30

Phe Ser Lys Gly Asp Arg Leu Gly Lys Val Ala Asp Trp Thr Gly Ala
 35 35 40 45

Thr Tyr Gln Asp Lys Arg Tyr Thr Asn Lys Tyr Ser Ser Gln Phe Gly
 50 55 60

40 Gly Gly Ser Gln Tyr Ala Tyr Phe His Glu Glu Asp Glu Ser Ser Phe
 65 70 75 80

Gln Leu Val Asp Thr Ala Arg Thr Gln Lys Thr Ala Tyr Gln Arg Asn
 85 90 95

45 Arg Met Arg Phe Ala Gln Arg Asn Leu Arg Arg Asp Lys Asp Arg Arg
 100 105 110

Asn Met Leu Gln Phe Asn Leu Gln Ile Leu Pro Lys Ser Ala Lys Gln
 115 120 125

50 Lys Glu Arg Glu Arg Ile Arg Leu Gln Lys Lys Phe Gln Lys Gln Phe
 130 135 140

Gly Val Arg Gln Lys Trp Asp Gln Lys Ser Gln Lys Pro Arg Asp Ser
 145 150 155 160

Ser Val Glu Val Arg Ser Asp Trp Glu Val Lys Glu Glu Met Asp Phe
 165 170 175

60 Pro Gln Leu Met Lys Met Arg Tyr Leu Glu Val Ser Glu Pro Gln Asp

	180	185	190
	Ile Glu Cys Cys Gly Ala Leu Glu Tyr Tyr Asp Lys Ala Phe Asp Arg		
	195	200	205
5	Ile Thr Thr Arg Ser Glu Lys Pro Leu Arg Xaa Xaa Lys Arg Ile Phe		
	210	215	220
	His Thr Val Thr Thr Thr Asp Asp Pro Val Ile Arg Lys Leu Ala Lys		
10	225	230	235 240
	Thr Gln Gly Asn Val Phe Ala Thr Asp Ala Ile Leu Ala Thr Leu Met		
	245	250	255
15	Ser Cys Thr Arg Ser Val Tyr Ser Trp Asp Ile Val Val Gln Arg Val		
	260	265	270
	Gly Ser Lys Leu Phe Phe Asp Lys Arg Asp Asn Ser Asp Phe Asp Leu		
20	275	280	285
	Leu Thr Val Ser Glu Thr Ala Asn Glu Pro Pro Gln Asp Glu Gly Asn		
	290	295	300
	Ser Phe Asn Ser Pro Arg Asn Leu Ala Met Glu Ala Thr Tyr Ile Asn		
25	305	310	315 320
	His Asn Phe Ser Gln Gln Cys Leu Arg Met Gly Lys Glu Arg Tyr Asn		
	325	330	335
30	Phe Pro Asn Pro Asn Pro Phe Val Glu Asp Asp Met Asp Lys Asn Glu		
	340	345	350
	Ile Ala Ser Val Ala Tyr Arg Tyr Arg Ser Gly Lys Leu Gly Asp Asp		
35	355	360	365
	Ile Asp Leu Ile Val Arg Cys Glu His Asp Gly Val Met Thr Gly Ala		
	370	375	380
	Asn Gly Glu Val Ser Phe Ile Asn Ile Lys Thr Leu Asn Glu Trp Asp		
40	385	390	395 400
	Ser Arg His Cys Asn Gly Val Asp Trp Arg Gln Lys Leu Asp Ser Gln		
	405	410	415
45	Arg Gly Ala Val Ile Ala Thr Glu Leu Lys Asn Asn Ser Tyr Lys Leu		
	420	425	430
	Ala Arg Trp Thr Cys Cys Ala Leu Leu Ala Gly Ser Glu Tyr Leu Lys		
50	435	440	445
	Leu Gly Tyr Val Ser Arg Tyr His Val Lys Asp Ser Ser Arg His Val		
	450	455	460
	Ile Leu Gly Thr Gln Gln Phe Lys Pro Asn Glu Phe Ala Ser Gln Ile		
55	465	470	475 480
	Asn Leu Ser Val Glu Asn Ala Trp Gly Ile Leu Arg Cys Val Ile Asp		
	485	490	495
60	Ile Cys Met Lys Leu Glu Glu Gly Lys Tyr Leu Ile Leu Lys Asp Pro		

500 505 510

Asn Lys Gln Val Ile Arg Val Tyr Ser Leu Pro Asp Gly Thr Phe Ser
 515 520 525

5 Ser

10 (2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 194 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

20 Lys Lys Arg His Thr Asp Val Gln Phe Tyr Thr Glu Val Gly Glu Ile
 1 5 10 15

Thr Thr Asp Leu Gly Lys His Gln His Met His Asp Arg Asp Asp Leu
 20 25 30

25 Tyr Ala Glu Gln Met Glu Arg Glu Met Arg His Lys Leu Lys Thr Ala
 35 40 45

Phe Lys Asn Phe Ile Glu Lys Val Glu Ala Leu Thr Lys Glu Glu Leu
 50 55 60

30 Glu Phe Glu Val Pro Phe Arg Asp Leu Gly Phe Asn Gly Ala Pro Tyr
 65 70 75 80

35 Arg Ser Thr Cys Leu Leu Gln Pro Thr Ser Ser Ala Leu Val Asn Ala
 85 90 95

Thr Glu Trp Pro Pro Phe Val Val Thr Leu Asp Glu Val Glu Leu Ile
 100 105 110

40 His Phe Xaa Arg Val Gln Phe His Leu Lys Asn Phe Asp Met Val Ile
 115 120 125

Val Tyr Lys Asp Tyr Ser Lys Lys Val Thr Met Ile Asn Ala Ile Pro
 130 135 140

45 Val Ala Ser Leu Asp Pro Ile Lys Glu Trp Leu Asn Ser Cys Asp Leu
 145 150 155 160

50 Lys Tyr Thr Glu Gly Val Gln Ser Leu Asn Trp Thr Lys Ile Met Lys
 165 170 175

Thr Ile Val Asp Asp Pro Glu Gly Phe Phe Glu Gln Gly Gly Trp Ser
 180 185 190

55 Phe Leu

60 (2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

Arg Ser Gly Leu Gly Leu Gly Ile Thr Ile Ala Phe Leu Ala Thr Leu
 1 5 10 15
 Ile Thr Gln Phe Leu Val Tyr Asn Gly Val Tyr Gln Tyr Thr Ser Pro
 20 25 30
 Asp Phe Leu Tyr Ile Arg Ser Trp Leu Pro Cys Ile Phe Phe Ser Gly
 35 40 45
 Gly Val Thr Val Gly Asn Ile Gly Arg Gln Leu Ala Met Gly Val Pro
 50 55 60
 Glu Lys Pro His Ser Asp
 65 70

(2) INFORMATION FOR SEQ ID NO: 641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser Val Glu
 1 5 10 15
 Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Xaa Xaa Pro Xaa
 20 25 30
 Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr
 35 40 45
 Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe
 50 55 60
 Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile Ser Asn
 65 70 75 80
 Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp
 85 90 95
 Thr Arg Arg Ser Gly
 100

(2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

5 Met Glu Ala Gln Gln Val Asn Glu Ala Glu Ser Ala Arg Glu Gln Leu
 1 5 10 15
 Gln Xaa Leu His Asp Gln Ile Ala Gly Gln Lys Ala Ser Lys Gln Glu
 20 25 30
 10 Leu Glu Thr Glu Leu Glu Arg Leu Lys Gln Glu Phe His Tyr Ile Glu
 35 40 45
 Glu Asp Leu Tyr Arg Thr Lys Asn Thr Leu Gln Ser Arg Ile Lys Asp
 50 55 60
 15 Arg Asp Glu Glu Ile Gln Lys Leu Arg Asn Gln Leu Thr Asn Lys Thr
 65 70 75 80
 20 Leu Ser Asn Ser Ser Gln Ser Glu Leu Glu Asn Arg Leu His Gln Leu
 85 90 95
 Thr Glu Thr Leu Ile Gln Lys Gln Thr Met Leu Glu Ser Leu Ser Thr
 100 105 110
 25 Glu Lys Asn Ser Leu Val Phe Gln Leu Glu Arg Leu Glu Gln Gln Met
 115 120 125
 Asn Ser Ala Ser Gly Ser Ser Ser Asn Gly Ser Ser Ile Asn Met Ser
 130 135 140
 30 Gly Ile Asp Asn Gly Glu Gly Thr Arg Leu Arg Asn Val Pro Val Leu
 145 150 155 160
 35 Phe Asn Asp Thr Glu Thr Asn Leu Ala Gly Met Tyr Gly Lys Val Arg
 165 170 175
 Lys Ala Ala Ser Ser Ile Asp Gln Phe Ser Ile Arg Leu Gly Ile Phe
 180 185 190
 40 Leu Arg Arg Tyr Pro Ile Ala Arg Val Phe Val Ile Ile Tyr Met Ala
 195 200 205
 Leu Leu His Leu Trp Val Met Ile Val Leu Leu Thr Tyr Thr Pro Glu
 210 215 220
 45 Met His His Asp Gln Pro Tyr Gly Lys
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

60 Ile Arg His Glu Gln His Pro Asn Phe Ser Leu Glu Met His Ser Lys
 1 5 10 15

Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile Leu Ile Leu Pro
20 25 30

5 Val Cys Ala His Leu His Glu Glu Leu Asn Cys
35 40

10 (2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

Ser Phe Phe Ile Ser Glu Glu Lys Gly His Leu Leu Leu Gln Ala Glu
1 5 10 15

20 Arg His Pro Trp Val Ala Gly Ala Leu Val Gly Val Ser Gly Gly Leu
20 25 30

25 Thr Leu Thr Thr Cys Ser Gly Pro Thr Glu Lys Pro Ala Thr Lys Asn
35 40 45

Tyr Phe Leu Lys Arg Leu Leu Gln Glu Met His Ile Arg Ala Asn
50 55 60

30

35

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97897
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

For receiving Office use only



This sheet was received with the international application

Authorized officer

Susan White
PCT International Division

For International Bureau use only



This sheet was received by the International Bureau on

Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209043
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For receiving Office use only</div> <div style="padding: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For International Bureau use only</div> <div style="padding: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>119</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 4, 1997	Accession Number 209235
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer Susan White PCT International Division</div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97898
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: right; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: right; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209044
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border: 1px solid black; padding: 2px; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px; min-height: 40px;">Authorized officer <div style="text-align: center; margin-top: 10px;">Susan White PCT International Division</div></div>	<div style="border: 1px solid black; padding: 2px; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; min-height: 40px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97899
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For receiving Office use only</div> <div style="padding: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For International Bureau use only</div> <div style="padding: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209045
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White POT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>130</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit April 28, 1997	Accession Number 209011
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97900
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97901
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209046
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="padding: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="padding: 10px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="padding: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="padding: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209047
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For receiving Office use only</div> <div style="padding: 10px;"><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer Susan White PCT International Division</div>	<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For International Bureau use only</div> <div style="padding: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 22, 1997	Accession Number 209076
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="padding: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="padding: 10px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="padding: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="padding: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>140</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (<i>including postal code and country</i>) 12301 Parklawn Drive Rockville, Maryland 20852 .. United States of America	
Date of deposit <u>August 21, 1997</u>	Accession Number <u>209215</u>
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)	
E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)	
The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i>)	

<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97904
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For receiving Office use only</div> <div style="padding: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer Susan White PCT International Division</div>	<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For International Bureau use only</div> <div style="padding: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>154</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>12301 Parklawn Drive Rockville, Maryland 20852 United States of America</p>	
Date of deposit <u>July 3, 1997</u>	Accession Number <u>209139</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<p style="text-align: center;">For receiving Office use only</p> <div><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div>Authorized officer Susan White PCT International Division</div>	<p style="text-align: center;">For International Bureau use only</p> <div><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div>Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209049
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center; margin-top: 10px;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97903
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit June 12, 1997	Accession Number 209119
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97902
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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(PCT Rule 13bis)

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209048
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209050
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
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Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 12, 1998</u>	Accession Number <u>209627</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

(f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

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6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

15

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

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9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

25

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

30

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

35

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the
5 full length protein comprises sequential amino acid deletions from either the C-terminus
or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of
claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim
11.

15. A method of making an isolated polypeptide comprising:
15 (a) culturing the recombinant host cell of claim 14 under conditions such that
said polypeptide is expressed; and
(b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition,
comprising administering to a mammalian subject a therapeutically effective amount of
the polypeptide of claim 11 or the polynucleotide of claim 1.

18. A method of diagnosing a pathological condition or a susceptibility to a
pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of
claim 1; and

(b) diagnosing a pathological condition or a susceptibility to a pathological
30 condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a
pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of
35 claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological
condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- (a) contacting the polypeptide of claim 11 with a binding partner; and
- 5 (b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

10 22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
- (b) isolating the supernatant;
- (c) detecting an activity in a biological assay; and
- 15 (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.

Applicant's or agent's file
reference number

PS001PCT

International application No. Unassigned

PCT US 08/04493

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

REC'D 03 APR 1998
WIPO PCT

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 26, 1997</u>	Accession Number <u>97904</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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Sergio J. de
la Hoz
International Laboratory

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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

Page 2

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

REC'D 03 APR 1998
WIPO

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>116</u>, line <u>N/A</u></p>	
<p>B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/></p>	
<p>Name of depositary institution <u>American Type Culture Collection</u></p>	
<p>Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u></p>	
<p>Date of deposit <u>May 15, 1997</u></p>	<p>Accession Number <u>209043</u></p>
<p>C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/></p>	
<p>In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>	
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)</p>	
<p>E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)</p>	
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PCT International Division

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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

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Page 2

UNITED KINGDOM

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DENMARK

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SWEDEN

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NETHERLANDS

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REC'D 03 APR 1998

WIPO PCT

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97897
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
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CANADA

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NORWAY

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SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 119, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 4, 1997	Accession Number 209235
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

Page 2

UNITED KINGDOM

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DENMARK

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SWEDEN

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NETHERLANDS

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>May 15, 1997</u>	Accession Number <u>209044</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Authorized officer <u>Susan White</u> <u>PCT International Division</u>	Authorized officer

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

Page 2

UNITED KINGDOM

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DENMARK

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SWEDEN

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NETHERLANDS

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REC'D 03 APR 1998

WIPO MICROORGANISM

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 26, 1997</u>	Accession Number <u>97898</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

Page 2

UNITED KINGDOM

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DENMARK

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SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

REC'D 03 APR 1998

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 126, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209045
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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PCT International Division

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CANADA

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NORWAY

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AUSTRALIA

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FINLAND

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Page 2

UNITED KINGDOM

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DENMARK

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NETHERLANDS

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 26, 1997</u>	Accession Number <u>97899</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
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PCT International Division

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CANADA

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FINLAND

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Page 2

UNITED KINGDOM

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DENMARK

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NETHERLANDS

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REC'D 03 APR 1998

WIPO PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>130</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>April 28, 1997</u>	Accession Number <u>209011</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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Page 2

UNITED KINGDOM

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DENMARK

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NETHERLANDS

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 131, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209046
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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PCT International Division

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CANADA

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REC'D 03 APR 1998

WIPO

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(PCT Rule 13bis)

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 26, 1997</u>	Accession Number <u>97900</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
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CANADA

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>May 22, 1997</u>	Accession Number <u>209076</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
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PCT International Division

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CANADA

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REC'D 03 APR 1998

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(PCT Rule 13bis)

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Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>May 15, 1997</u>	Accession Number <u>209047</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
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REC'D 03 APR 1998

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Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97901
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 140, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit August 21, 1997	Accession Number 209215
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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PCT International Division

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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

Page 2

UNITED KINGDOM

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DENMARK

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SWEDEN

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NETHERLANDS

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description

on page 142, line N/A

B. IDENTIFICATION OF DEPOSIT

Further deposits are identified on an additional sheet ☒

Name of depositary institution American Type Culture Collection

Address of depositary institution (including postal code and country)

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit June 12, 1997

Accession Number 209119

C. ADDITIONAL INDICATIONS (leave blank if not applicable)

This information is continued on an additional sheet ☐

In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)

E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)

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PCT International Division

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CANADA

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NORWAY

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AUSTRALIA

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FINLAND

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Page 2

UNITED KINGDOM

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DENMARK

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SWEDEN

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NETHERLANDS

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 12, 1998</u>	Accession Number <u>209627</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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Page 2

UNITED KINGDOM

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DENMARK

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SWEDEN

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NETHERLANDS

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 146, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209048
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g. "Accession Number of Deposit")	
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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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Page 2

UNITED KINGDOM

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DENMARK

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SWEDEN

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NETHERLANDS

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REC'D 03 APR 1998

WIPO PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 26, 1997</u>	Accession Number <u>97902</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
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Susan White
PCT International Division

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CANADA

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NORWAY

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FINLAND

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Page 2

UNITED KINGDOM

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>May 15, 1997</u>	Accession Number <u>209049</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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CANADA

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NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

Page 2

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description
on page 153, line N/A

B. IDENTIFICATION OF DEPOSIT

Further deposits are identified on an additional sheet ☒

Name of depositary institution American Type Culture Collection

Address of depositary institution (including postal code and country)

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit February 26, 1997

Accession Number 97903

C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet ☐

In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)

E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)

The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")

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Susan White
PCT International Division

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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

Page 2

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

DENMARK

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SWEDEN

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NETHERLANDS

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>154</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>July 3, 1997</u>	Accession Number <u>209139</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
For receiving Office use only	
<input checked="" type="checkbox"/> This sheet was received with the international application	For International Bureau use only
Authorized officer <u>Susan White</u> <u>PCT International Division</u>	<input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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FINLAND

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Page 2

UNITED KINGDOM

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REC'D 03 APR 1998

WIPO

PCT

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>May 15, 1997</u>	Accession Number <u>209050</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="border: 1px solid black; padding: 5px;"><div style="text-align: right; margin-bottom: 5px;">For receiving Office use only</div><div style="display: flex; align-items: center;"><input checked="" type="checkbox"/> This sheet was received with the international application</div><div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer Susan White PCT International Division</div></div>	<div style="border: 1px solid black; padding: 5px;"><div style="text-align: right; margin-bottom: 5px;">For International Bureau use only</div><div style="display: flex; align-items: center;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div><div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer</div></div>

CANADA

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NORWAY

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